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From: Slobodyansky, Elizabeth
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Elizabeth Slobodyansky, PhD

Primary Examiner

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Patent Family: _____
Other: _____

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OM protein - protein search, using sw model

Run on: August 5, 2004, 13:09:29 ; Search time 54 Seconds
(without alignments) 617.419 Million cell updates/sec

Title: US-09-430-029-8

Perfect score: 63.9

Sequence: 1 MDAGGVCGTVTAQTDERRA.....RLRKPFCCGACAGTAINK 118

Scoring table: BL0SUM62

Gapext 10.0 , Gapext 0.5

Searched: 1586107 seqs, 283547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:
1: geneseqP1980s:*

2: geneseqP1990s:*

3: geneseqP2000s:*

4: geneseqP2001s:*

5: geneseqP2002s:*

6: geneseqP2003as:*

7: geneseqP2003bs:*

8: geneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
ID AAY84822 standard; protein; 118 AA.

XX
AC AAY84822;
XX DT 08-AUG-2000 (first entry)
DE Amino acid sequence of toluene monooxygenase TomQ.
XX Toluene monooxygenase; TomK; TomL; TomM; TomO; TomP; toluene; ortho-cresol; 3-methylcatachol; chlorinated compound; aliphatic hydrocarbon; trichloroethylene; dichloroethylene; phenol; KW aromatic compound; benzene; cresol; environmental remediation.

XX OS Burkholderia cepacia.
XX PN EP999274-A2.
XX PD 10-MAY-2000.
XX PF 02-NOV-1999;
XX PR 30-OCT-1998;
XX PA (CAND) CANON RR.
XX PI Yano T, Nomoto T, Immamura T;
XX DR WPI; 2000-306010/27.
XX N-PSDB; AAA14845.

Claim 46: Page 45; 52pp; English.
AY84816-22 represent toluene monooxygenase enzymes TomK, TomL, TomM, TomN, TomO, TomP, and TomQ, respectively. The enzymes oxidise toluene to ortho-cresol and 3-methylcatechol. The toluene monooxygenase has a high efficiency in degrading aromatic and volatile organic chlorinated compounds. The nucleic acids are useful for the recombinant production of toluene monooxygenase. Toluene monooxygenase is useful for degrading a chlorinated aliphatic hydrocarbon compound (e.g. trichloroethylene (TCE) or dichloroethylene (DCE)), or an aromatic compound (e.g. toluene, benzene, phenol, and cresol), e.g. in environmental remediation. It is especially useful for purifying air polluted with chlorinated aliphatic

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	61.9	100.0	AAV84822	AY84822 Amino aci
2	41.8	67.6	AAV96262	AAV96262 R. eutrop
3	32.2	52.0	AAO23395	Aao23395 Pseudomon
4	259.5	41.9	AA646662	Aag646662 Hydroxykin
5	228.9	36.9	AAW989716	Aaw989716 Alcaligen
6	144.5	23.3	AAR66216	Aar66216 Nocardi
7	144.5	23.3	RA881472	Aar81472 Nocardi
8	130.0	21.1	ABP22750	Abp22750 Protein e
9	129.5	20.9	AAW80338	Aaw80338 Oxidase e
10	126.5	20.4	ABU21309	Abu21309 Protein e
11	124.5	20.1	ABU19841	Abu19841 Protein e
12	123	19.9	ABP97021	Abp97021 Sphingomo
13	123	19.9	ABP97025	Abp97025 Sphingomo
14	120	19.4	ABU41589	Abu41589 Protein e
15	117	18.9	ABU40068	Abu40068 Protein e
16	113	18.3	ABU38911	Abu38911 Protein e
17	111	17.9	ABP79217	N. gonorr
18	110	17.8	AAW14449	AAw14449 Carb gene
19	109.5	17.7	ABP78930	Abp78930 N. gonorr
20	109.5	17.7	ABU37353	Abu37353 Protein e
21	109	17.6	ABP22973	Abp22973 Protein e
22	105	17.0	AAR05385	Aar05385 Xylene ox
23	104.5	17.0	ABP97023	Abp97023 Pseudomon
24	104.5	16.9	ABE60228	Aab60228 Pseudomon
25	103.5	16.7	AAG92388	C glutami

CC hydrocarbon compounds
 XX Sequence 118 AA;
 SQ

Query Match 100.0%; Score 619; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 1.5e-63;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDAGRVGCTTIAQTDERYACTVSGESLLAGMAKLRGKIPVCGVCKVVRVLGAVRKLGPISR 60
 1 MDAGRVGCTTIAQTDERYACTVSGESLLAGMAKLRGKIPVCGVCKVVRVLGAVRKLGPISR 60

Qy 1 RKLGPITSRAHVSAAEENDGYALACRVPDGDVELEAVGRLRKPFQGMACAGTAINK 118
 61 RKLGPITSRAHVSAAEENDGYALACRVPDGDVELEAVGRLRKPFQGMACAGTAINK 118
 61 RKLGPITSRAHVSAAEENDGYALACRVPDGDVELEAVGRLRKPFQGMACAGTAINK 118

Db

RESULT 2
 AAY96262
 ID AAY96262 standard; protein; 111 AA.
 XX
 AAY96262;
 AC
 XX
 12-SEP-2003 (revised)
 DT 11-SEP-2000 (first entry)
 XX
 R. eutropha toluene monooxygenase TomQ polypeptide.
 XX Toluene monooxygenase; carcinogen; halogenated aliphatic hydrocarbon;
 KW halogenated aromatic hydrocarbon; environmental pollution; TomQ;
 KW environmental remediation; enzyme.
 XX
 OS Ralstonia eutropha; strain TB64.
 EN EP1006191-A2.
 XX
 ED 07-JUN-2000.
 XX
 PF 03-DEC-1999; 99EP-00124209.
 XX
 PR 03-DEC-1998; 9BJP-00344506.
 XX
 PA (CANO) CANON KK.
 XX
 PI Yano T, Nonoto T, Imaura T;
 XX
 DR WPI; 2000-378265/33.
 XX
 DR ; AAA:0292.
 XX
 New polynucleotide encoding toluene monooxygenase for generating
 PT transformants useful for decontaminating environments polluted with e.g.
 PR aromatic hydrocarbons.
 XX
 Claim 38; Page 48; 54PP; English.
 XX
 The present sequence is the Ralstonia eutropha toluene monooxygenase TomQ
 CC polypeptide. This peptide is encoded by a DNA fragment of about 5.3 Kb
 CC which also contains six other coding sequences encoding other toluene
 CC monooxygenase polypeptides (AAA:0292). The DNA fragment is useful for
 CC transforming microbial cells to confer them with toluene monooxygenase
 CC activity. These cells are in turn useful for decontaminating environments
 CC polluted with halogenated aliphatic compounds e.g. tetrachloroethylene
 CC (PCE), trichloroethylene (TCE) and dichloroethylene (DCE) and/or aromatic
 CC hydrocarbons e.g. toluene, benzene, phenol, cresol. These pollutants are
 CC considered to be potential carcinogens. The present sequence is not
 CC essential for toluene monooxygenase activity. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 XX
 Sequence 111 AA;
 SQ

Qy 9 TVTAQTDERYACTVSGESLLAGMAKLRGKIPVCGVCKVVRVLGAVRKLGPISR 68
 8 TVRAQTDERYACTVSGESLLAGMAKLRGKIPVCGVCKVVRVLGAVRKLGPISR 67

Db

Qy 69 AHVSAEEENDGYALACRVPDGDVELEAVGRLRKPFQGMACAGTAINK 111
 68 AHVSAEEENDGYALACRVPDGDVELEAVGRLRKPFQGMACAGTAINK 107

Db

RESULT 3
 AAO23395
 ID AAO23395 standard; protein; 119 AA.
 XX
 AAO23395;

XX
 06-NOV-2003 (first entry)
 XX
 Pseudomonas plasmid CT14 ORF1 bacterial ferredoxin protein.
 DE
 XX
 Bacterial plasmid; CT14; aromatic degradation; mercury; ferredoxin; ORF1.
 KW
 KW catechol; toluene degradative pathway; mercury; ferredoxin;
 XX
 OS Pseudomonas sp.
 XX
 PN US6548292-B1.
 XX
 PA 15-APR-2003.
 XX
 PR 20-NOV-2000; 2000US-00716865.
 XX
 PR 23-NOV-1999; 99US-0167062P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Bramucci MG, Chen NW, Nagarajan V;
 XX
 DR WPI; 2003-566606/53.
 DR N-PSDB; AAU56814.
 XX
 New bacterial plasmid isolated from Pseudomonas CT14, designated as
 PT CT14, useful for degrading aromatic compounds, and in plasmid
 PT replication, or partitioning of replicated plasmids to daughter cells
 PT during cell division.
 XX
 PS Example 4; Col 31-34; 60PP; English.
 XX
 This invention relates to a novel isolated bacterial plasmid designated
 CC CT14, isolated from a wastewater bacterial Pseudomonas strain.
 CC Specifically, the plasmid pCT14 carries the genes necessary for
 CC replication and stability in a host, as well as genes encoding enzymes
 CC for the degradation of various aromatic substrates including catechols
 CC and other intermediates in the toluene degradative pathway. Furthermore,
 CC the pCT14 carries heavy metal resistance genes and is useful for reducing the
 CC level of mercury in a contaminated environment. As for other bacterial
 CC plasmids, pCT14 also carries genes that are used for plasmid replication,
 CC partitioning of replicated plasmids to daughter cells during cell
 CC division and transposition of insertion sequences or transposons. This
 CC polypeptide sequence is the Pseudomonas CT14 ORF1 ferredoxin protein,
 CC which reactivates the catechol dioxygenase enzyme encoded by ORF2 of the
 CC invention.
 XX
 SQ Sequence 119 AA;
 XX
 Query Match 52.0%; Score 322; DB 7; Length 119;
 Best Local Similarity 56.4%; Pred. No. 3.6e-29;
 Matches 62; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

Qy 9 TVTAQTDERYACTVSGESLLAGMAKLRGKIPVCGVCKVVRVLGAVRKLGPISR 68
 10 SVHMQTGETFPATIDESLQGMURLRGKIPVCGVCKVVRVLGAVRKLGPISR 69

Db

Qy 69 AHVSAEEENDGYALACRVPDGDVELEAVGRLRKPFQGMACAGTAINK 118

Db 70 AHVSAABEARGFITLACRVAAPVTPVQLEVVGKFRKEVKVFSSTNRLINK 119
 RESULT 4
 AAG64662
 ID AAG64662 standard; protein; 112 AA.
 AC AAG64662;
 XX DT 14-SEP-2001 (first entry)
 XX DE Hydroxyindol-related protein #7.
 XX Xanthomonas maltophilia; 7-hydroxyindol; 7-hydroxytryptophan; drug;
 KW dyestuff; reagent.
 XX OS Stenotrophomonas maltophilia.
 XX PN JP2001095577-A.
 XX PD 10-APR-2001.
 XX PP 28-SEP-1999; 99JP-00273961.
 XX PR 28-SEP-1999; 99JP-00273961.
 XX PA (SARC) MERCIAN CORP.
 PA WPI; 2001-370201/39.
 DR N-PSDB; AAH45588.
 PT New Xanthomonas maltophilia DNA sequence, useful in a method for
 producing 7-hydroxyindol and 7-hydroxytryptophan which are useful as raw
 materials for drugs, dyestuffs and reagents.
 Disclosure; Page 16; 23pp; Japanese.
 CC This invention relates to a Stenotrophomonas maltophilia (Xanthomonas
 maltophilia) DNA sequence which encodes 9 proteins. The invention includes
 a method for the production of 7-hydroxyindol and 7-hydroxytryptophan in
 which a microbe carrying a fragment of the DNA sequence is capable of
 hydroxylating the 7-position of indol is cultured. The DNA is useful in a
 method for producing 7-hydroxyindol and 7-hydroxytryptophan which are
 useful as raw materials for drugs, dyestuffs and reagents. The present
 sequence represents a protein encoded by the DNA of the invention
 XX Sequence 112 AA;
 SQ Query Match 41.9%; Score 259.5; DB 4; Length 112;
 Best Local Similarity 50.5%; Prod. No. 5.7e-22;
 Matches 4 9; Conservative 17; Mismatches 30; Indels 1; Gaps 1;
 Qy 9 TVTIAQTDERYACVSGESELAGMAKLRGRGIPVGCLNGCGVCKVRKLVLRGAVRK 102
 Db 11 TVSLVTESEFQRDGETLQMLGRKGKIPGCLNGCGICKVHLAGF-EGGAMSR 68
 Qy 69 AHVSAEETENDGYALACVPPDGSIVELVEYAGRKPKFF 105
 Db 70 AHVCEDDVCHGVVLACRARPRTDVLKVGMCNSVF 106
 RESULT 5
 AAW98976
 ID AAW98976 standard; protein; 101 AA.
 AC AAW98976;
 XX DT 10-MAY-1999 (first entry)
 XX DE Alcaligenes sp. protein PoxG.
 XX KW Alcaligenes; PoxR; PoxA; PoxB; PoxC; PoxD; PoxE; PoxF; PoxG; PoxH; PoxI;
 PT Alkene monooxygenase and corresp. gene - useful for the epoxidation of an
 alkene.

XX aromatic; oxidative; petroleum purification; chemical industry; drug.
 XX OS Alcaligenes sp.
 XX PN JP11042088-A.
 XX PD 16-FEB-1999.
 XX PF 25-JUL-1997; 97JP-00200625.
 XX PR 25-JUL-1997; 97JP-00200625.
 XX PA (TOFU) TONEN CORP.
 XX DR WPI; 1999-197020/17.
 XX DR N-PSDB; AAX18867.
 XX PT New encoding an aromatic cpd. oxidative decompn. enzyme - useful in the
 fields of petroleum purification, chemical and drug industries.
 XX PT
 XX PS Claim 1; Page 7-19; 35pp; Japanese.
 XX CC The present sequence encodes Alcaligenes sp. protein PoxG. The present
 invention also describes PoxA, PoxB, PoxC, PoxD, PoxE, PoxF, PoxH, FoxH
 and PoxI. The proteins are useful in the fields of petroleum
 purification, chemical industry and drug industry related to the
 synthesis, conversion and decomposition of aromatic compounds
 XX CC
 XX SQ Sequence 101 AA;
 Query Match 36.9%; Score 228.5; DB 2; Length 101;
 Best Local Similarity 48.9%; Prod. No. 2e-18;
 Matches 46; Conservative 12; Mismatches 35; Indels 1; Gaps 1;
 PT
 XX Qy 9 TVTIAQTDERYACVSGESELAGMAKLRGRGIPVGCLNGCGVCKVRKLVLRGAVRK 102
 3 TVEIADSGQRYPGCDPQNLIRAMEVLGORGIPGCRGGCGVCKVRITESGRYR-TGKNSR 68
 Db 69 AHVSAEETENDGYALACVPPDGSIVELVEYAGRK 102
 62 ACLESBEOQGGLVIAKRAFPDSDIRLRAALLAR 95
 RESULT 6
 AAK66216
 ID AAK66216 standard; protein; 342 AA.
 XX AC AAK66216;
 XX AC AAK66216;
 XX DT 16-OCT-2003 (revised)
 DT 04-AUG-1995 (first entry)
 XX DE Nocardia corallina reductase (encoded by amod).
 XX KW alkene monooxygenase; reductase; epoxidase; amod.
 XX XX Gordonia rubripertinctus.
 XX PN JP06292571-A.
 XX PD 21-OCT-1994.
 XX PF 06-APR-1993; 93JP-00105171.
 XX PR 06-APR-1993; 93JP-00105171.
 XX PA (NIHA) JAPAN ENERGY CORP.
 XX DR WPI; 1995-009039/02.
 DR N-PSDB; AAQ79559.
 XX PT Alkene monooxygenase and corresp. gene - useful for the epoxidation of an
 alkene.

CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX Sequence 343 AA;

Query Match 20.4%; Score 126.5; DB 6; Length 343;
 Best Local Similarity 35.4%; Pred. No. 5.5e-06;
 Matches 34; Conservative 15; Mismatches 34; Indels 13; Gaps 4;

QY 10 VTTAQDTDERYACVSGESLIAAGMALKLGRGIPVGCLNGGCCVCKYVRLGAVRKLGPIRSA 69
 5 VTLRSQGRQFOVEQDEPVLSALRQ-TIGLYGCNGACGSCKGTIVSGETEQ---RA 58

QY 70 H---VSAEEENDGYALACRVVPGDGYEL---EVAG 98

DB 59 HSSSALSNEEKTGRMALFCATACTDLEVDIREVAG 94

RESULT 11
 ABU19841 standard; protein; 343 AA.
 ID ABU19841 standard; protein; 343 AA.
 XX
 AC ABU19841;
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #5368.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS Borrelia cepacia.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX EF 21-MAR-2002; 2002WO-US009107.
 XX FR 21-MAR-2001; 2001US-00815342.
 BR 06-SEP-2001; 2001US-00948393.
 PR 25-OCT-2001; 2001US-0342933P.
 PR 08-FEB-2002; 2002US-00072551.
 PR 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Hasselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI: 2003-029926/02.
 DR N-PSDB; ACA23711.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 47765; 1766PP; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway; (8)
 CC requiring a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufaturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic form directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX Sequence 343 AA;

Query Match 20.1%; Score 124.5; DB 6; Length 343;
 Best Local Similarity 32.6%; Pred. No. 9.4e-06;
 Matches 30; Conservative 20; Mismatches 37; Indels 5; Gaps 3;

QY 10 VTTAQDTDERYACVSGESLIAAGMALKLGRGIPVGCLNGGCCVCKYVRLGAVRKLGPIRSA 69
 5 VTLRSQGRQFOVEQDEPVLSALRQ-TIGLYGCNGACGSCKGTIVSGETEQ---RA 58

QY 70 HVSAAEENDGYALACRVVPGDGYEL---EVAG 98

DB 63 ALSNDERTRGILALLCCSKAQCDELEIDVREIAG 94

RESULT 12
 ABP97021
 ID ABP97021 standard; protein; 346 AA.
 XX
 AC ABP97021;
 XX DT 18-JUN-2003 (first entry)
 XX Spingomonas strain ASU1 xylA protein SEQ ID NO:12.
 DE XX
 KW Xylene monooxygenase; substituted monocyclic aromatic compound; enzyme;
 KW Oxidation; biocatalytic; xylM; xylA; 4-hydroxymethylbenzoic acid; film;
 KW 3-hydroxymethylbenzoic acid; p-toluic acid; p-tolualdehyde; polyester;
 KW 4-methylbenzyl alcohol; m-toluic acid; 3-methylbenzyl alcohol; fibre;
 KW m-tolualdehyde; paint; adhesive; beverage container.
 XX Spingomonas sp.
 OS XX
 PN WO2003014368-A2.
 XX
 PD 20-FEB-2003
 XX PF 09-AUG-2002; 2002WO-US027106.
 XX PR 10-AUG-2001; 2001US-0311490P.
 XX
 PI (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (BRAM/) BRAMUCCI M G.
 PA (NAGA/) NAGARAJAN V.
 PA (THOM/) THOMAS S M.
 XX
 PI Bramucci MG, Nagarajan V, Thomas SM;
 XX WPI; 2003-354403/33.
 DR N-PSDB; ACC9113.
 XX
 PT Oxidizing substituted monocyclic aromatic substrate, by contacting
 PT recombinant microorganism having DNA fragment encoding xylE
 PT monooxygenase enzyme comprising xylA and xylM subunits, with the
 PT substrate.
 XX

PS Claim 11; Page 64-65; 70pp; English.
 XX The present invention describes a method for oxidising a substituted monocyclic aromatic substrate (I). The method involves contacting a recombinant microorganism comprising a DNA fragment encoding a xylene monooxygenase enzyme comprising a xylA subunit and a xylM subunit, with (I), or contacting a xylene monooxygenase enzyme comprising a xylA subunit and a xylM subunit in vitro with (I). The method can be used for oxidising a substituted monocyclic aromatic substrate, especially for producing 4-hydroxymethylbenzoic acid, 3-hydroxymethylbenzoic acid, p-toluic acid, p-tolualdehyde, 4-methylbenzyl alcohol, m-toluic acid, m-toluinaldehyde or 3-methylbenzyl alcohol. The compounds produced are useful as monomers in the production of polyesters used in fibres, films, paints, adhesives and beverage containers. The method is cost-effective and produces fewer environmentally harmful waste products. The present sequence represents xylA isolated from *Sphingomonas* strain ASU1, which is used in an example from the present invention.

XX Sequence 346 AA;
 PS Query Match 19.9%; Score 123; DB 6; Length 346;
 XX Best Local Similarity 30.1%; Pred. No. 1.4e-05;
 XX Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;

QY 9 TVTIAQTDERYACVSGESLILAGMAKLGRRGIPVGCLNGGGVCKVRVLGAVRKIGPISR 68
 DB 12 TVTVEGSPPTLDIAGKTLEAMLDAG-LAMPHDKVGSCTFKLVSGKIGLSPSL 70
 QY 69 AHVSAEEENDGYALACRVVGDVEVAGRLRKPFCCGMACA 111
 DB 71 A-LEGDELLSGFRLACQAIPLRSIDLIAVDA---PLSQGIAIA 108
 RESULT 13
 AC ABB97025 standard; protein; 346 AA.
 AC ABB97025;
 XX 18-JUN-2003 (first entry)
 DE *Sphingomonas* pNL1 xylA protein SEQ ID NO:22.
 XX Xylene monooxygenase; substituted monocyclic aromatic compound; enzyme; oxidation; biocatalytic; xylM; xylA; 4-hydroxymethylbenzoic acid; film; 3-hydroxymethylbenzoic acid; p-toluic acid; p-tolualdehyde; polyester; 4-methylbenzyl alcohol; m-toluic acid; 3-methylbenzyl alcohol; fibre; m-toluinaldehyde; paint; adhesive; beverage container.
 XX Novosphingobium aromaticivorans.
 OS
 PN WO2003014368-A2.
 XX 20-FEB-2003.
 PD 09-AUG-2002; 2002WO-US027106.
 PP
 XX 10-AUG-2001; 2001US-0311490P.
 PR
 XX (DUPO) DU PONT DE NEOMOURS & CO E I.
 PA (BRAMUCCI M G.
 PA (NAGA/) NAGARAJAN V.
 PA (THOM/) THOMAS S M.
 XX
 PI Bramucci MG, Nagarajan V, Thomas SM;
 XX WPI; 2003-354403/33.
 DR N-PSDB; ACC49120.
 XX
 PT Oxidising substituted monocyclic aromatic substrate, by contacting recombinant microorganism having DNA fragment encoding xylene monooxygenase enzyme comprising xylA and xylM subunits, with the substrate.

PS Claim 11; Page 70pp; English.
 XX The present invention describes a method for oxidising a substituted monocyclic aromatic substrate (I). The method involves contacting a recombinant microorganism comprising a DNA fragment encoding a xylene monooxygenase enzyme comprising a xylA subunit and a xylM subunit, with (I), or contacting a xylene monooxygenase enzyme comprising a xylA subunit and a xylM subunit in vitro with (I). The method can be used for oxidising a substituted monocyclic aromatic substrate, especially for producing 4-hydroxymethylbenzoic acid, 3-hydroxymethylbenzoic acid, p-toluic acid, p-tolualdehyde, 4-methylbenzyl alcohol. The compounds produced are useful as monomers in the production of polyesters used in fibres, films, paints, adhesives and beverage containers. The method is cost-effective and produces fewer environmentally harmful waste products. The present sequence represents xylA isolated from *Sphingomonas* pNL1, which is used in an example from the present invention. N.B. The present sequence is not given in the specification, as the specification does not appear to be complete, but is derived from Genbank accession number AF079317 (see page 7).
 XX Sequence 346 AA;
 SQ Query Match 19.9%; Score 123; DB 6; Length 346;
 XX Best Local Similarity 30.1%; Pred. No. 1.4e-05;
 XX Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;
 SQ Sequence 346 AA;

QY 9 TVTIAQTDERYACVSGESLILAGMAKLGRRGIPVGCLNGGGVCKVRVLGAVRKIGPISR 68
 DB 12 TVTVEGSPPTLDIAGKTLEAMLDAG-LAMPHDKVGSCTFKLVSGKIGLSPSL 70
 QY 9 TVTIAQTDERYACVSGESLILAGMAKLGRRGIPVGCLNGGGVCKVRVLGAVRKIGPISR 68
 DB 12 TVTVEGSPPTLDIAGKTLEAMLDAG-LAMPHDKVGSCTFKLVSGKIGLSPSL 70
 QY 69 AHVSAEEENDGYALACRVVGDVEVAGRLRKPFCCGMACA 111
 DB 71 A-LEGDELLSGFRLACQAIPLRSIDLIAVDA---PLSQGIAIA 108
 RESULT 14
 ID ABU41589 standard; protein; 366 AA.
 XX ABU41589;
 AC ABU41589;
 XX 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #27116.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Pseudomonas* syringae.
 XX WO200277183-A2.
 XX 03-OCT-2002.
 XX 21-MAR-2002; 2002WO-US009107.
 PR
 XX (ELITR-) ELITRA PHARM INC.
 PR
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PR Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA,
 PR
 XX DR 2003-029924/02.
 PR N-PSDB; ACA45459.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to

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OM protein - protein search, using sw model.

Run on: August 5, 2004, 13:04:13 ; Search time 18 Seconds (without alignments)

Title: US-09-430-029-8

Perfect score: 6.19

Sequence: 1 MDAGRVCIGTTIAQTDERYA.....RLRKFFFCGMACAGTTAAINK 118

Scoring table: BLOSUM62

Gapext 0.5

Searched: 389414 seqs, 5165971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	418.5	67.6	111	4	US-09-453-956-8	Sequence 8, Appli
2	322	52.0	119	4	US-09-716-865-2	Sequence 2, Appli
3	144.5	23.3	342	1	US-08-499-215-5	Sequence 5, Appli
4	113	18.3	391	4	US-09-252-991A-17118	Sequence 17118, A
5	111	17.9	387	4	US-09-489-039A-14027	Sequence 14027, A
6	110	17.8	92	2	US-08-737-825-7	Sequence 7, Appli
7	104.5	16.9	326	6	51-71684-7	Patent No. 5171684
8	103	16.6	353	4	US-09-543-681A-7190	Sequence 7190, AP
9	96	15.5	358	4	US-09-328-352-6375	Sequence 6375, AP
10	94.5	15.3	411	4	US-09-543-681A-5480	Sequence 5480, AP
11	92.5	14.9	339	4	US-09-489-039A-12074	Sequence 12074, A
12	91	14.7	377	4	US-09-489-039A-9429	Sequence 9429, AP
13	90.5	14.6	431	4	US-09-198-452A-952	Sequence 952, AP
14	88	14.2	352	4	US-09-453-956-7	Sequence 7, Appli
15	88	14.2	381	4	US-09-489-039A-12111	Sequence 12111, A
16	88	14.2	390	4	US-09-543-681A-7837	Sequence 7837, AP
17	85	13.7	348	4	US-09-252-991A-31249	Sequence 31249, A
18	85	13.7	416	4	US-09-540-236-2215	Sequence 2215, AP
19	84.5	13.7	360	4	US-09-252-991A-23023	Sequence 23023, A
20	83.5	13.5	348	4	US-09-328-352-6843	Sequence 6843, AP
21	83	13.4	411	4	US-09-489-039A-12676	Sequence 12676, A
22	79.5	12.8	351	4	US-08-319-387-6	Sequence 6, Appli
23	78.5	12.7	524	4	US-09-252-991A-27006	Sequence 27006, A
24	77	12.4	425	4	US-09-252-991A-29520	Sequence 29520, A
25	76	12.3	139	4	US-09-252-991A-25753	Sequence 25753, A
26	76	12.3	403	4	US-09-252-991A-25706	Sequence 25706, A
27	76	12.3	424	4	US-09-252-991A-18548	Sequence 18548, A

ALIGNMENTS

RESULT 1
US-09-453-956-8

; Sequence 8, Application US/09453956

; GENERAL INFORMATION:

; APPLICANT: Yano, Tetsuya; No. 64721910to, Tsuyoshi; Immura, Takeshi; Patent No. 6472191

; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monoxygenase Gene, Recombinant Plasmid, Transformed Microorganism, Method for Degrading Halogenated Aliphatic Hydrocarbon

; TITLE OF INVENTION: Method for Environmental Remediation

; FILE REFERENCE: CFI014074US

; CURRENT APPLICATION NUMBER: US/09/453,956

; CURRENT FILING DATE: 1999-12-03

; EARLIER APPLICATION NUMBER: JP P1998-344506

; EARLIER FILING DATE: 1998-12-03

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 111

; TYPE: PRT

; ORGANISM: Ralstonia eutropha

; FEATURE: Other Information: TomQ polypeptide

US-09-453-956-8

Query Match 9, Conservative 79; Mismatches 12; Indels 3; Gaps 1;

Query 9 TTVTAQTDERYACVGSBSLLAGNAKLRGTPVGCGNGGCYCKVYLRGAVRKLGPIISR 68

Best Local Similarity 76.7%; Pred. No. 2e-42;

Matches 79; Conservati 9; Mismatches 12; Indels 3; Gaps 1;

Db 8 TTVVAQTCESPTAGSLLAAGLRRGTFVGCNNGGCYCKVYLRGAVRKLGPIISR 67

Qy 69 AHVSAEENDGYALACRVAQVDPGDVELEVAGRLRKPFPCGMACA 111

Db 68 AHVSADEBGLGTYLACRVAQVDPDVLEVAGRMQKPLC--CA 107

RESULT 2
US-09-716-865-2

; Sequence 2, Application US/09716865

; Patent No. 6518292

; GENERAL INFORMATION:

; APPLICANT: Bramucci, Michael G

; APPLICANT: Nagarajan, Vasanth

; APPLICANT: Chen, Mario W.

; TITLE OF INVENTION: Bacterial Plasmid Having Genes Encoding Enzymes for the Degradation of Aromatic Compounds

; TITLE OF INVENTION: Degradation of Aromatic Compounds

FILE REFERENCE: BC1016 US NA

CURRENT APPLICATION NUMBER: US/09/716,865

PRIOR APPLICATION NUMBER: 2000-11-26

PRIOR FILING DATE: 2000-11-26

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Microsoft Office 97

SEQ ID NO 2

TYPE: PRT

ORGANISM: *Pseudomonas* CT14

US-09-716-865-2

Query Match 52.0%; Score 322; DB 4; Length 119;

Best Local Similarity 56.4%; Pred. No. 7e-31; Gaps 0;

Matches 62; Conservative 13; Mismatches 35; Indels 0;

QY 9 TTYIAQTDERYACVSGESLLAGMALKGRGGTIPVGCLNGGGCVKVRVLGAVRKLGKPISR 68

Db 10 SVEWQMTGHTPCTADESLLQGMRLGRKGKIPVGCVNGCGVCKVHIVLGQCRPLGPVSR 69

QY 69 AHYSAEEENDGYALACRVPDGDVLEYAGRLLRKPFECGACAGTAINK 118

Db 70 AHYSAEEARGFTIACRVPDGDVLEYAGRLLRKPFECGACAGTAINK 119

US-09-252-991A-17118

RESULT 4

US-09-252-991A-17118

; Sequence 17118, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES FOR DIAGNOSTICS AND THERAPY

; FILE REFERENCE: 107196-1136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 17118

; LENGTH: 391

; TYPE: PRT

; ORGANISM: *Pseudomonas aeruginosa*

US-09-252-991A-17118

Query Match 18.3%; Score 113; DB 4;

Best Local Similarity 37.3%; Pred. No. 2.8e-05;

Matches 28; Conservative 12; Mismatches 25;

Inde-

QY 24 GESLJPGMAKLGRRGTPVGCLNGGGCVKVRVLGAVRKLGKPISR 68

Db 323 GETVHAAKGLH-TPKACGMGICGTCKV-----MKTAGEVEMM

QY 81 ALACRVTVPDGDVLE 95

Db 376 ILSCCSVPKGDVVID 390

US-09-489-039A-14027

RESULT 5

US-09-489-039A-14027

; Sequence 14027, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES FOR DIAGNOSTICS AND THERAPY

; FILE REFERENCE: 2709-2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 14027

; LENGTH: 387

; TYPE: PRT

; ORGANISM: *Klebsiella pneumoniae*

US-09-489-039A-14027

Query Match 17.9%; Score 111; DB 4;

Best Local Similarity 35.8%; Pred. No. 4.7e-05;

Matches 34; Conservative 13; Mismatches 40;

Inde-

QY 9 TTYIAQTD-ERYACVSGE--SLLAGMALKGRGGTIPVGCLNGGGCVKVRVLGAVRKLGKPISR 68

Db 294 TVTIRQDGRDLIALSAEDDSLDAILRQG-ADLPAFKGGVCATG

QY 66 ISRAHTSAEEENDGYALACRVPDGDVLEVAGR 99

Db 353 Y\$-----LEADELAAGYVLSQCQSLPTSGDVYVDFDAR 384

US-08-499-215-5

Query Match 23.3%; Score 144.5; DB 1;

Best Local Similarity 38.6%; Pred. No. 4.1e-09;

Matches 39; Conservative 13; Mismatches 44; Indels 5; Gaps 4;

QY 9 TTYIAQTDERYACVSGESLLAGMALKGRGGTIPVGCLNGGGCVKVRVLGAVRKLGKPISR 68

Db 3 TINQPFSHSYSECBGESLSDG-ALRNLSSLLKYGKHHGGTCKVRLDDVEEPGS-SP 60

US-09-252-991A-17118

RESULT 6

US-08-737-825-7
 Sequence 7, Application US/08737825
 Patent No. 587192
 GENERAL INFORMATION
 APPLICANT: SALMONID, GEORGE PEACOCK COPELAND
 APPLICANT: MCGOWAN, SIMON JAMES
 APPLICANT: SEBATHIA, MOHAMMED
 APPLICANT: COX, ANTHONY RICHARD JOHN
 APPLICANT: HOLDEN, MATTHEW THOMAS GEOFFREY
 APPLICANT: PORTER, LAUREN ELIZABETH
 APPLICANT: BYCROFT, BARRIE WALSHAM
 APPLICANT: WILLIAMS, PAUL
 APPLICANT: STEWART, GORDON SIDNEY ANDERSON BIRNIE
 TITLE OF INVENTION: GENES INVOLVED IN THE BIOSYNTHETIC PATHWAY OF CARBAPENEM
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESS: Birch, Stewart, Kolasch & Birch, LLP
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22400-0747

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MICROSOFT WORD 97

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/737,825
 FILING DATE: 03-07-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: SVENSSON, LEONARD R.
 REGISTRATION NUMBER: 30,330
 REFERENCE/DOCKET NUMBER: 1009-0105P
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 TELE: 248345
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 92 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Erwinia carotovora
 US-08-737-825-7

Query Match 25 ESSLAGMALKRGRGIPVGCLNGGCVKVRGAVR --KLGPISRAHSAEEENDGYA 82
 Best Local Similarity 39.7%; Pred. No. 1e-05; Indels 8; Gaps 3;
 Matches 29; Conservative 11; Mismatches 25; Indels 8; Gaps 3;

Query 25 ESSLAGMALKRGRGIPVGCLNGGCVKVRGAVR --KLGPISRAHSAEEENDGYA 82
 Db 21 ESYLSSAYEAGVB-LPTRCAGTCGVCVRRLTSGNVNMDSGGISRKDA ---DGYL 74

Query 83 ACRVVPDDEVE 95
 Db 75 PCCSVPLSNLEIE 87

RESULT 7
 5171684-7
 ; Patent No. 5171684
 ; TITLE OF INVENTION: YEN, KWANG-MU;BLATT, LAWRENCE M.;KARL, MICHAEL R.
 ; MONOOXYGENASE OF PSEUDOMONAS MENDOCINA KR-1
 ; NUMBER OF SEQUENCES: 41
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/590,374

Query Match 15.5%; Score 96; DB 4; Length 358;

Best Local Similarity 30.9%; Pred. No. 0.0026; Matches 25; Conservative 12; Mismatches 32; Indels 12; Gaps 3; SEQ ID NO: 543-681A-5480

QY 10 VTIQDTERVACVSGESULLAGMAKLGRRGIPVGCLNGCGVCKVRVLGAVRKLGPISSRA 69
DB 281 VSVAQDD-----ESTILDAALRAG-ADLPYACKGGCATCRCKVLSGEVDMFLNYS-- 329

QY 70 HVAEAEFENDGYALACRVPDGG 90
DB 330 -LEEDVEKGYVLSCLTPKG 349

RESULT 10
US-09-543-681A-5480
i Sequence 5480, Application US/09543681A
i Patent No. 6610836
i GENERAL INFORMATION:
i APPLICANT: GARY BRETON
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
i TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
i FILE REFERENCE: 2709-1002-001
i CURRENT APPLICATION NUMBER: US/09/543,681A
i CURRENT FILING DATE: 2000-04-05
i PRIORITY NUMBER: US 60/128,706
i PRIOR FILING DATE: 1999-04-09
i SEQ ID NO: 5480
i LENGTH: 411
i TYPE: PRT
i ORGANISM: Proteus mirabilis
US-09-543-681A-5480

Query Match 15.3%; Score 94.5%; DB 4; Length 411;
Best Local Similarity 32.1%; Pred. No. 0.0047; Matches 27; Conservative 17; Mismatches 33; Indels 7; Gaps 4; SEQ ID NO: 5480

QY 16 DERYACVSGESULLAGMAKLGRRGIPV-GCLNGG-CGVCKVRVLGAVRKLGPISSRAHVS 72
DB 47 EKSFHAPGDKIL---NVLSNEGQCRVYKQCRVYKQLEGGDIL-PTELSHIN 102

QY 73 AEEENDGYALACRVPDGGDVELEV 96
DB 103 KREAKEGCRLACQVNNTKNLKEL 126

RESULT 11
US-09-489-039A-12074
i Sequence 12074, Application US/09489039A
i Patent No. 6610836
i GENERAL INFORMATION:
i APPLICANT: Gary Breton et. al
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
i FILE REFERENCE: 2709-2004001
i CURRENT APPLICATION NUMBER: US/09/489,039A
i CURRENT FILING DATE: 2000-01-27
i PRIOR APPLICATION NUMBER: US 60/117,747
i LENGTH: 339
i TYPE: PRT
i ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12074

Query Match 14.9%; Score 92.5%; DB 4; Length 339;
Best Local Similarity 35.9%; Pred. No. 0.0065; Matches 28; Conservative 10; Mismatches 35; Indels 5; Gaps 3; SEQ ID NO: 5480

QY 17 ERYACVSGESULLAGMAKLGRRGIPVGCLNGCGVCKVRVLGAVRKLGPISSRAHVS 76
DB 266 ERYAPV-GTTLDAL-ESNKVPTVACRAGVCGCCKTUVSG--KYSVSTSTMILDAEI 320

QY 77 NDGYALACRVPDGGDVEL 94
DB 321 ADGYVLAACSPHSDILV 338

RESULT 12
US-09-489-039A-9429
i Sequence 9429, Application US/09489039A
i Patent No. 6610836
i GENERAL INFORMATION:
i APPLICANT: Gary Breton et. al
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
i FILE REFERENCE: 2709-040001
i CURRENT FILING DATE: 2000-01-27
i PRIORITY NUMBER: US 60/117,747
i PRIOR FILING DATE: 1999-01-29
i NUMBER OF SEQ ID NOS: 14342
i SEQ ID NO: 9429
i LENGTH: 377
i TYPE: PRT
i ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9429

Query Match 14.7%; Score 91%; DB 4; Length 377;
Best Local Similarity 29.7%; Pred. No. 0.011; Mismatches 27; Indels 4; Gaps 3;

QY 9 TVTIACTDERYACVSGESULLAGMAKLGRRGIPVGCLNGCGVCKVRVLGAVRKLGPI-S 67
DB 290 TITLASTGERMP-VPODKTIAQVQLEHGAVPLSCEMGICGACTLPVREGTVDRDVTQVS 348

Query Match 14.7%; Score 91%; DB 4; Length 377;
Best Local Similarity 29.7%; Pred. No. 0.011; Mismatches 27; Indels 4; Gaps 3;

QY 68 RAHVSAAEENDGYALACRVPDGGDVELEVAG 98
DB 349 EAEKQAAEQH--IACCSRSLSANLVIDLAG 377

RESULT 13
US-09-198-452A-952
i Sequence 952, Application US/09198452A
i Patent No. 6559294
i GENERAL INFORMATION:
i APPLICANT: Griffelis, R
i TITLE OF INVENTION: chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
i FILE REFERENCE: 9710-003-939
i CURRENT APPLICATION NUMBER: US/09/198,452A
i CURRENT FILING DATE: 1998-11-24
i NUMBER OF SEQ ID NOS: 6849
i SEQ ID NO: 952
i LENGTH: 431
i TYPE: PRT
i ORGANISM: Chlamydia pneumoniae
US-09-198-452A-952

Query Match 14.6%; Score 90.5%; DB 4; Length 431;
Best Local Similarity 32.5%; Pred. No. 0.015; Mismatches 26; Indels 7; Gaps 3;

QY 23 SGESULLAGMAKLGRRGIPVGCLNGG--CGYCKVRLGAVRKLGPISSRAHVS 79
DB 57 SGQTLVSLLS--SGTIPSPCGGKATROCKVRRVKNADEPL-ETDRSTFSKROOLEG 112

QY 80 YALACRVPDGGDVELEVAGR 99
DB 113 WRLSCQCKVQHDMSLIEER 132

RESULT 14
US-09-453-956-7
i Sequence 7, Application US/09453956

Patent No. 6472191
 APPLICANT: Yano, Tetsuya; No. 6472191;oto, Tsuyoshi; Tamura, Takeshi;
 TITLE OF INVENTION: DNA Fragment Carrying Toluene Monoxygenase Gene,
 TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
 TITLE OF INVENTION: Method for Degrading Halogenated Aliphatic Hydrocarbon
 TITLE OF INVENTION: Compounds and Aromatic Compounds, and
 TITLE OF INVENTION: Method for Environmental Remediation
 FILE REFERENCE: CPO14074US
 CURRENT APPLICATION NUMBER: US/09/453,956
 CURRENT FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: JP P1998-344506
 PRIOR FILING DATE: 1998-12-03
 NUMBER OF SEQ ID NOS: 14
 SEQ ID NO: 7
 SOFTWARE: Patentin Ver. 2.1
 LENGTH: 352
 TYPE: PRT
 ORGANISM: Ralstonia eutropha
 FEATURE:
 OTHER INFORMATION: TomP polypeptide
 US-09-453-956-7

Query Match 14.2%; Score 88; DB 4; Length 352;
 Best Local Similarity 34.7%; Pred. No. 0.023; Mismatches 9; Indels 2; Gaps 2;
 Matches 25; Conservative 9; Matches 2; Indels 2; Gaps 2;

Qy 24 GESLLAGMAKLGRGRGIPVGCLNGGGVCKVRLGAVRKLGPIRSRAHVSAAEENDGYALA 83
 Db 19 GQTILDAARQGIV-IPHACCHGLGTCVKSVLDGEA-DLGEANPFLMDFEREGKALA 76

Qy 84 CRVYPPDGIVLE 95
 Db 77 CCATLQADTTIE 88

RESULT 15
 US-09-489-039A-12111
 Sequence 12111, Application US/09489039A
 Patent No. 6610816
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2739 2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 12111
 LENGTH: 381
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-12111

Query Match 14.2%; Score 88; DB 4; Length 381;
 Best Local Similarity 31.2%; Pred. No. 0.026; Mismatches 14; Indels 8; Gaps 3;
 Matches 25; Conservative 18; Matches 33; Indels 8; Gaps 3;

Qy 9 TTVIAQTDERYACVSGESLLAGMAKLGRGRGIPVGCLNGGGVCKVRLGAVRKLGPIRS 68
 Db 302 TVALIEWQGQFTGNQNVILEQQGIR-VPYSCRAGIGSCRIRLBBGEV--SPLKK 357

Qy 69 AHVSAEEENDGYALACRVYP 88
 Db 358 NAVA---GDTGTLIACSCVP 373

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Gencore version 5.1.6

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Run on: August 5, 2004, 13:08:34 ; Search time 46 Seconds (without alignments)

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Score: 804.665 Million cell updates/sec

Title: US-09-430-029-8

Perfect score: 619

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Total number of hits satisfying chosen parameters: 1291235

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Maximum DB seq length: 20000000000

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18: /cgn2_6/ptodata/1/pubpa/US60_NEW_PUB.pep:*

Post-processing: Maximum Match 10%

Listing First 45 summaries

Database : Published Applications AA:*

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYA. RLRKPFCCG MACAGTAANK 118

Score: 804.665 Million cell updates/sec

16 105 17.0 105 14 US-10-213-878-18

17 105 17.0 105 14 US-10-214-059-18

18 103.5 16.7 103.5 12 US-10-425-114-4745

19 103.5 16.7 103.5 9 US-09-738-626-6142

20 103 16.6 103 12 US-10-282-122A-68779

21 103 16.6 103 12 US-10-282-122A-49831

22 101.5 16.4 101.5 12 US-10-282-122A-65847

23 101 16.3 101 12 US-10-282-122A-53556

24 100 16.2 100 12 US-10-282-122A-48031

25 99 16.0 99 12 US-10-282-122A-77980

26 94.5 15.3 94.5 14 US-10-156-761-11884

27 92.5 14.9 92.5 12 US-10-282-122A-59569

28 92.5 14.9 92.5 12 US-10-282-122A-49127

29 91.5 14.8 91.5 12 US-10-282-122A-75961

30 90.5 14.6 90.5 12 US-10-282-122A-54966

31 90.5 14.6 90.5 15 US-10-289-767-952

32 90 14.5 90 12 US-10-282-122A-50665

33 89.5 14.5 89.5 12 US-10-282-122A-42942

34 89 14.4 89 12 US-10-224-599-150076

35 88 14.2 88 14 US-10-223-371B-7

36 87 14.1 87 12 US-10-282-122A-55785

37 86.5 14.0 86.5 15 US-10-282-122A-55074

38 84.5 13.7 84.5 16 US-10-437-963-133198

39 84.5 13.7 84.5 12 US-10-282-122A-66811

40 82 13.2 82 12 US-10-282-122A-69345

41 81 13.1 81 9 US-09-430-029-7

42 80.5 13.0 80.5 15 US-10-216-464-31

43 79.5 12.8 79.5 12 US-10-282-122A-44836

44 78.5 12.7 78.5 12 US-10-425-114-66819

45 78.5 12.7 78.5 12 US-10-425-114-67176

ALIGNMENTS

RESULT 1 US-09-430-029-8

; Sequence 8, Application US-094300029

; GENERAL INFORMATION:

; APPLICANT: Yano, Tetsuya; No. US20020168738A1oto, tsuyoshi; Imamura, Takeshi; Canon 1

; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,

; TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,

; TITLE OF INVENTION: Method for Degrading Chlorinated Aliphatic Hydrocarbon

; TITLE OF INVENTION: Compounds and Aromatic Compounds, and

; TITLE OF INVENTION: Method for Environmental Remediation

; FILE REFERENCE: CPO13982US

; CURRENT APPLICATION NUMBER: US-09/430-029

; CURRENT FILING DATE: 1599-10-29

; EARLIER APPLICATION NUMBER: JP P1998-310801

; EARLIER FILING DATE: 1598-10-30

; NUMBER OF SEQ ID: NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 8

; LENGTH: 118

; TYPE: PRT

; ORGANISM: Burkholderia cepacia

; FEATURE:

; OTHER INFORMATION: TomQ polypeptide

US-09-430-029-8

Query Match 100.0%; Score 619; DB 9; Length 118;

Best Local Similarity 100.0%; Pred. No. 6.8e-0; Mismatches 0; Indels 0; Gaps 0;

Matches 118; Conservative 100.0%;

Qy 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Db 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

2 41.8 5 67.6 111 14 US-10-223-371B-8

3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9 346 14 US-10-214-059-12

8 123 19.9 346 14 US-10-214-059-12

9 123 19.9 346 14 US-10-214-059-12

10 120 19.4 366 12 US-10-282-122A-679513

11 117 18.9 368 12 US-10-282-122A-67952

12 113 18.3 366 12 US-10-282-122A-66835

13 109.5 17.7 336 12 US-10-282-122A-65277

14 109 17.6 348 12 US-10-282-122A-50897

15 105.5 17.0 169 12 US-10-424-599-275773

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

2 41.8 5 67.6 111 14 US-10-223-371B-8

3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9 346 14 US-10-214-059-12

8 123 19.9 346 14 US-10-214-059-12

9 123 19.9 346 14 US-10-214-059-12

10 120 19.4 366 12 US-10-282-122A-679513

11 117 18.9 368 12 US-10-282-122A-67952

12 113 18.3 366 12 US-10-282-122A-66835

13 109.5 17.7 336 12 US-10-282-122A-65277

14 109 17.6 348 12 US-10-282-122A-50897

15 105.5 17.0 169 12 US-10-424-599-275773

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

2 41.8 5 67.6 111 14 US-10-223-371B-8

3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9 346 14 US-10-214-059-12

8 123 19.9 346 14 US-10-214-059-12

9 123 19.9 346 14 US-10-214-059-12

10 120 19.4 366 12 US-10-282-122A-679513

11 117 18.9 368 12 US-10-282-122A-67952

12 113 18.3 366 12 US-10-282-122A-66835

13 109.5 17.7 336 12 US-10-282-122A-65277

14 109 17.6 348 12 US-10-282-122A-50897

15 105.5 17.0 169 12 US-10-424-599-275773

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

2 41.8 5 67.6 111 14 US-10-223-371B-8

3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9 346 14 US-10-214-059-12

8 123 19.9 346 14 US-10-214-059-12

9 123 19.9 346 14 US-10-214-059-12

10 120 19.4 366 12 US-10-282-122A-679513

11 117 18.9 368 12 US-10-282-122A-67952

12 113 18.3 366 12 US-10-282-122A-66835

13 109.5 17.7 336 12 US-10-282-122A-65277

14 109 17.6 348 12 US-10-282-122A-50897

15 105.5 17.0 169 12 US-10-424-599-275773

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

2 41.8 5 67.6 111 14 US-10-223-371B-8

3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9 346 14 US-10-214-059-12

8 123 19.9 346 14 US-10-214-059-12

9 123 19.9 346 14 US-10-214-059-12

10 120 19.4 366 12 US-10-282-122A-679513

11 117 18.9 368 12 US-10-282-122A-67952

12 113 18.3 366 12 US-10-282-122A-66835

13 109.5 17.7 336 12 US-10-282-122A-65277

14 109 17.6 348 12 US-10-282-122A-50897

15 105.5 17.0 169 12 US-10-424-599-275773

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

2 41.8 5 67.6 111 14 US-10-223-371B-8

3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9 346 14 US-10-214-059-12

8 123 19.9 346 14 US-10-214-059-12

9 123 19.9 346 14 US-10-214-059-12

10 120 19.4 366 12 US-10-282-122A-679513

11 117 18.9 368 12 US-10-282-122A-67952

12 113 18.3 366 12 US-10-282-122A-66835

13 109.5 17.7 336 12 US-10-282-122A-65277

14 109 17.6 348 12 US-10-282-122A-50897

15 105.5 17.0 169 12 US-10-424-599-275773

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

2 41.8 5 67.6 111 14 US-10-223-371B-8

3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9 346 14 US-10-214-059-12

8 123 19.9 346 14 US-10-214-059-12

9 123 19.9 346 14 US-10-214-059-12

10 120 19.4 366 12 US-10-282-122A-679513

11 117 18.9 368 12 US-10-282-122A-67952

12 113 18.3 366 12 US-10-282-122A-66835

13 109.5 17.7 336 12 US-10-282-122A-65277

14 109 17.6 348 12 US-10-282-122A-50897

15 105.5 17.0 169 12 US-10-424-599-275773

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

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3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9 346 14 US-10-214-059-12

8 123 19.9 346 14 US-10-214-059-12

9 123 19.9 346 14 US-10-214-059-12

10 120 19.4 366 12 US-10-282-122A-679513

11 117 18.9 368 12 US-10-282-122A-67952

12 113 18.3 366 12 US-10-282-122A-66835

13 109.5 17.7 336 12 US-10-282-122A-65277

14 109 17.6 348 12 US-10-282-122A-50897

15 105.5 17.0 169 12 US-10-424-599-275773

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

2 41.8 5 67.6 111 14 US-10-223-371B-8

3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9 346 14 US-10-214-059-12

8 123 19.9 346 14 US-10-214-059-12

9 123 19.9 346 14 US-10-214-059-12

10 120 19.4 366 12 US-10-282-122A-679513

11 117 18.9 368 12 US-10-282-122A-67952

12 113 18.3 366 12 US-10-282-122A-66835

13 109.5 17.7 336 12 US-10-282-122A-65277

14 109 17.6 348 12 US-10-282-122A-50897

15 105.5 17.0 169 12 US-10-424-599-275773

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

2 41.8 5 67.6 111 14 US-10-223-371B-8

3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9 346 14 US-10-214-059-12

8 123 19.9 346 14 US-10-214-059-12

9 123 19.9 346 14 US-10-214-059-12

10 120 19.4 366 12 US-10-282-122A-679513

11 117 18.9 368 12 US-10-282-122A-67952

12 113 18.3 366 12 US-10-282-122A-66835

13 109.5 17.7 336 12 US-10-282-122A-65277

14 109 17.6 348 12 US-10-282-122A-50897

15 105.5 17.0 169 12 US-10-424-599-275773

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

2 41.8 5 67.6 111 14 US-10-223-371B-8

3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9 346 14 US-10-214-059-12

8 123 19.9 346 14 US-10-214-059-12

9 123 19.9 346 14 US-10-214-059-12

10 120 19.4 366 12 US-10-282-122A-679513

11 117 18.9 368 12 US-10-282-122A-67952

12 113 18.3 366 12 US-10-282-122A-66835

13 109.5 17.7 336 12 US-10-282-122A-65277

14 109 17.6 348 12 US-10-282-122A-50897

15 105.5 17.0 169 12 US-10-424-599-275773

Scoring table: BL050M62

Gapop 10.0 , Gapext 0.5

Score: 804.665 Million cell updates/sec

Sequence: 1 MDAGRVCSTYIAQTDERYACYSGESLLAGMAKLRGQIPYGCLNGCGVCKVRVRGAV 60

Score: 804.665 Million cell updates/sec

1 61.9 100.0 118 9 US-09-430-029-8

2 41.8 5 67.6 111 14 US-10-223-371B-8

3 130.5 21.1 343 12 US-10-282-122A-50674

4 124.5 20.4 343 12 US-10-282-122A-49233

5 124.5 20.1 343 12 US-10-282-122A-47765

6 123 19.9 346 14 US-10-213-878-12

7 123 19.9

Query Match 20.4%; Score 126.5; DB 12; Length 343; Best Local Similarity 35.4%; Pred. No. 4.4e-06; Matches 34; Conservative 15; Mismatches 34; Indels 13; Gaps 4; Result 6

Qy 10 VTIATQDERYACVSGESLLAGMAKLRGGIPVGCLNGGCCVCKYVRLGAVRKLGPISR 69
Db 5 VTLKQSGRQFQVESSETVLAALRQNH-LPYGCNGACGSCKGGIVSGIEQ-GPHAA 62

Qy 70 H---VSAEFFNDGYALACRVPDQVEL--EVAG 98
Db 59 HSSSALSNEEKTRGMALFCCATACTDLEVDIREVAG 94

Result 5

US-10-282-122A-47765
Sequence 47765, Application US/10282122A
Publication No. US20040029129A1
General Information
Applicant: Wang, Liangsu
Applicant: Zamudio, Carlos
Applicant: Malone, Cherry
Applicant: Haselbeck, Robert
Applicant: Zyskind, Kari
Applicant: Wall, Daniel
Applicant: Trawick, John
Applicant: Yamamoto, Robert
Applicant: Forsyth, R.
Xu, H.

Title of Invention: Identification of Essential Genes in Microorganisms
Current Application Number: US/10/282,122A
Current Filing Date: 2003-02-20
Prior Filing Date: 2000-03-21
Prior Application Number: 60/191,078
Prior Filing Date: 2000-05-23
Prior Application Number: 60/207,727
Prior Filing Date: 2000-05-26
Prior Application Number: 60/230,335
Prior Filing Date: 2000-09-06
Prior Application Number: 60/230,347
Prior Application Number: 60/242,578
Prior Filing Date: 2000-10-23
Prior Application Number: 60/253,625
Prior Filing Date: 2000-11-27
Prior Application Number: 60/257,931
Prior Application Number: 60/267,636
Prior Filing Date: 2001-02-09
Prior Application Number: 60/269,308
Prior Filing Date: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
Number of SEQ ID NOS: 78614
Software: PatentIn version 3.1
SEQ ID NO 47765
Length: 343
Type: PRT
Organism: Burkholderia cepacia
US-10-282-122A-47765

Qy 10 VTIATQDERYACVSGESLLAGMAKLRGGIPVGCLNGGCCVCKYVRLGAVRKLGPISR 69
Db 5 VTLKQSGRQFQVESSETVLAALRQNH-LPYGCNGACGSCKGGIVSGIEQ-GPHAA 62

Qy 70 HVSABEENDGYALACRVPDQVEL--EVAG 98
Db 63 ALSNDETRGLALLCSKAQCDLETDVRETAG 94

Result 6

Query Match 19.9%; Score 123; DB 14; Length 346; Best Local Similarity 30.1%; Pred. No. 1.1e-05; Mismatches 46; Indels 6; Gaps 3;

Qy 9 TVTIATQDERYACVSGESLLAGMAKLRGGIPVGCLNGGCCVCKYVRLGAVRKLGPISR 68
Db 12 TVTVEGSPPTLDIPAGKTLLEMLDAG-LAMPHDCVKVSGCTKFKLVSGKIGELSPSAL 70

Qy 69 AHVSAEFFNDGYALACRVPDQVELEVAGRRLRKFFFGCMACA 111
Db 71 A-LEDDELSGFRLACQAIPRSDLTAVDA---PLSOGIATA 108

Result 7

US-10-213-878-22
Sequence 22, Application US/10213878
Publication No. US20030073206A1
General Information
Applicant: Bramucci, Michael
Applicant: Nagarajan, Vasantha
Applicant: Thomas, Stuart
Title of Invention: Monooxygenase for the Oxidation of Substituted Monocyclic Aromatic Compounds
File Reference: CL1662 US NA
Current Application Number: US/10/213,878
Prior Application Number: 60/311,490
Prior Filing Date: 2001-08-10
Number of SEQ ID NOS: 22
SEQ ID NO 12
Software: Microsoft Office 97
Length: 346
Type: PRT
Organism: Sphingomonas sp.
US-10-213-878-22

Query Match 19.9%; Score 123; DB 14; Length 346; Best Local Similarity 30.1%; Pred. No. 1.1e-05; Mismatches 46; Indels 6; Gaps 3;

Qy 9 TVTIATQDERYACVSGESLLAGMAKLRGGIPVGCLNGGCCVCKYVRLGAVRKLGPISR 68

RESULT 8
 US-10-214-059-12
 ; Sequence 12, Application US/10214059
 ; Publication No. US2003007778A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bramucci, Michael
 ; APPLICANT: Nagarajan, Vasanth
 ; TITLE OF INVENTION: Use of Xylene Monooxygenase for the Oxidation of Substituted
 ; POLYCYCLIC Aromatic Compounds
 ; FILE REFERENCE: CL1663 US NA
 ; CURRENT APPLICATION NUMBER: US/10/214,059
 ; CURRENT FILING DATE: 2002-08-07
 ; PRIOR APPLICATION NUMBER: 60/311,486
 ; PRIOR FILING DATE: 2001-08-10
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 12
 ; LENGTH: 346
 ; TYPE: PRT
 ; ORGANISM: Sphingomonas sp.
 US-10-214-059-12

Query Match 19.9%; Score 123; DB 14; Length 346;
 Best Local Similarity 30.1%; Pred. No. 1.1e-05; Indels 6; Gaps 3;
 Matches 31; Conservative 20; Mismatches 46;

Db 9 TTVIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCCYCKVRVLRGAVRKPLGPISR 68
 12 TVTVEGGSPPTLDIPAGKTLEAMLDAG-LAMPHDKVSGCTCKFVLVSGKIGELSPSAL 70

Qy 69 AHVSAEEENDGYALACRVRVPDGVLEVAGRLRKPFEGMACA 111
 Db 71 A-LEGDELRSGFRLACQAIQPRSLTIAVDA---PLSQGIATA 108

RESULT 10
 US-10-282-122A-69513
 ; Sequence 69513, Application US/10282122A
 ; Publication No. US2004002129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Hasselbeck, Robert
 ; APPLICANT: Ohlsken, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forbush, R.
 ; Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA-034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 69513
 ; LENGTH: 366
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas syringae
 US-10-282-122A-69513

Query Match 19.4%; Score 120; DB 12; Length 366;
 Best Local Similarity 37.2%; Pred. No. 2.7e-05
 Matches 32; Conservative 9; Mismatches 41; Indels 4; Gaps 2;

Db 10 VTTIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCCYCKVRVLRGAVRKPLGPISR 69
 284 VEFIDTGSIRVAGETVAAARKLGIM-IPRAGMGCTGTRVMKLSGEVEM--EHNG 339

Qy 70 HVSAEEENDGYALACRVRVPDGVLE 95
 Db 340 GITTEDVAEGYIILUSCCSVPKGDRVIE 365

RESULT 11
 US-10-282-122A-67992
 ; Sequence 67992, Application US/10282122A

Query Match 19.9%; Score 123; DB 14; Length 346;
 Best Local Similarity 30.1%; Pred. No. 1.1e-05; Indels 6; Gaps 3;
 Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;
 SEQ ID NO 22
 LENGTH: 346
 TYPE: PRT
 ; ORGANISM: Sphingomonas sp.
 US-10-214-059-22

Query Match 19.9%; Score 123; DB 14; Length 346;
 Best Local Similarity 30.1%; Pred. No. 1.1e-05; Indels 6; Gaps 3;
 Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;
 SEQ ID NO 22

Qy 9 TTVIAQTDERYACVSGESLLAGMAKLGRRGIPVGCLNGGCCYCKVRVLRGAVRKPLGPISR 68
 Db 340 GITTEDVAEGYIILUSCCSVPKGDRVIE 365

Publication No. US20040029129A1
 GENERAL INFORMATION
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA-03A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIORITY NUMBER: 60/191,078
 PRIORITY FILING DATE: 2000-03-21
 PRIORITY APPLICATION NUMBER: 60/206,848
 PRIORITY FILING DATE: 2000-05-23
 PRIORITY APPLICATION NUMBER: 60/207,727
 PRIORITY FILING DATE: 2000-05-26
 PRIORITY APPLICATION NUMBER: 60/230,335
 PRIORITY FILING DATE: 2000-09-06
 PRIORITY APPLICATION NUMBER: 60/230,344
 PRIORITY FILING DATE: 2000-09-09
 PRIORITY APPLICATION NUMBER: 60/242,578
 PRIORITY FILING DATE: 2000-10-23
 PRIORITY APPLICATION NUMBER: 60/253,625
 PRIORITY FILING DATE: 2000-11-27
 PRIORITY APPLICATION NUMBER: 60/257,931
 PRIORITY FILING DATE: 2000-12-22
 PRIORITY APPLICATION NUMBER: 60/267,626
 PRIORITY FILING DATE: 2001-02-09
 PRIORITY APPLICATION NUMBER: 60/269,308
 PRIORITY FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 67635
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-10-282-122A-66635

Query Match 18.3% Score 113; DB 12; Length 366;
 Best Local Similarity 37.3%; Pred. No. 0.00018;
 Matches 28; Conservative 12; Mismatches 25; Indels 10; Gaps 3

Qy 24 GESLILAGMAKLGRGRGIPVGCLNGGCVKVRVLGAVRKLGPISRHVSABENDGVALA 83
 Db 298 GETVHAAAKLGLH-IPKACGMGICCTCKVLKLGGVEM--EHNGGTTPEDEAFYIS 355
 Qy 81 ALACRYYPDGYEL 95
 Db 351 IDSCCSVBRGDVVD 365

RESULT 13
 US-10-282-122A-65277
 ; Sequence 65277, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA-034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIORITY NUMBER: 60/191,078
 ; PRIORITY FILING DATE: 2000-03-20
 ; PRIORITY APPLICATION NUMBER: 60/206,848
 ; PRIORITY FILING DATE: 2000-05-23
 ; PRIORITY APPLICATION NUMBER: 60/207,727
 ; PRIORITY FILING DATE: 2000-05-26
 ; PRIORITY APPLICATION NUMBER: 60/230,335
 ; PRIORITY FILING DATE: 2000-09-06
 ; PRIORITY APPLICATION NUMBER: 60/230,344
 ; PRIORITY FILING DATE: 2000-09-09
 ; PRIORITY APPLICATION NUMBER: 60/242,578
 ; PRIORITY FILING DATE: 2000-10-23
 ; PRIORITY APPLICATION NUMBER: 60/253,625
 ; PRIORITY FILING DATE: 2000-11-27
 ; PRIORITY APPLICATION NUMBER: 60/257,931
 ; PRIORITY FILING DATE: 2000-12-22
 ; PRIORITY APPLICATION NUMBER: 60/267,626
 ; PRIORITY FILING DATE: 2001-02-09
 ; PRIORITY APPLICATION NUMBER: 60/269,308
 ; PRIORITY FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 67635
 ; TYPE: PRT
 ; ORGANISM: *Pseudomonas aeruginosa*
 ; US-10-282-122A-66635

Query Match 18.9% Score 117; DB 12; Length 368;
 Best Local Similarity 40.3%; Pred. No. 6.1e-05;
 Matches 29; Conservative 10; Mismatches 29; Indels 4; Gaps 2;

Qy 24 GESLILAGMAKLGRGRGIPVGCLNGGCVKVRVLGAVRKLGPISRHVSABENDGVALA 83
 Db 300 GETVHAAAKLGLH-IPKACGMGICCTCKVLKLGGVEM--EHNGGTTPEDEAFYIS 355

Query Match 18.3% Score 113; DB 12; Length 368;
 Best Local Similarity 40.3%; Pred. No. 6.1e-05;
 Matches 29; Conservative 10; Mismatches 29; Indels 4; Gaps 2;

Qy 84 CRVVPDGDYEL 95
 Db 356 CCSVPFKGDYRID 367

RESULT 12
 US-10-282-122A-66635
 ; Sequence 66635, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA-034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIORITY NUMBER: 60/191,078
 ; PRIORITY FILING DATE: 2000-03-20
 ; PRIORITY APPLICATION NUMBER: 60/206,848
 ; PRIORITY FILING DATE: 2000-05-23
 ; PRIORITY APPLICATION NUMBER: 60/207,727
 ; PRIORITY FILING DATE: 2000-05-26
 ; PRIORITY APPLICATION NUMBER: 60/230,335
 ; PRIORITY FILING DATE: 2000-09-06
 ; PRIORITY APPLICATION NUMBER: 60/230,344
 ; PRIORITY FILING DATE: 2000-09-09
 ; PRIORITY APPLICATION NUMBER: 60/242,578
 ; PRIORITY FILING DATE: 2000-10-23
 ; PRIORITY APPLICATION NUMBER: 60/253,625
 ; PRIORITY FILING DATE: 2000-11-27
 ; PRIORITY APPLICATION NUMBER: 60/257,931
 ; PRIORITY FILING DATE: 2000-12-22
 ; PRIORITY APPLICATION NUMBER: 60/267,636
 ; PRIORITY FILING DATE: 2001-02-09
 ; PRIORITY APPLICATION NUMBER: 60/269,308
 ; PRIORITY FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 67635
 ; TYPE: PRT
 ; ORGANISM: *Pseudomonas putida*
 ; US-10-282-122A-67992

Query Match 18.9% Score 117; DB 12; Length 368;
 Best Local Similarity 40.3%; Pred. No. 6.1e-05;
 Matches 29; Conservative 10; Mismatches 29; Indels 4; Gaps 2;

Qy 24 GESLILAGMAKLGRGRGIPVGCLNGGCVKVRVLGAVRKLGPISRHVSABENDGVALA 83
 Db 300 GETVHAAAKLGLH-IPKACGMGICCTCKVLKLGGVEM--EHNGGTTPEDEAFYIS 355

Query Match 18.9% Score 117; DB 12; Length 368;
 Best Local Similarity 40.3%; Pred. No. 6.1e-05;
 Matches 29; Conservative 10; Mismatches 29; Indels 4; Gaps 2;

Qy 84 CRVVPDGDYEL 95
 Db 356 CCSVPFKGDYRID 367

; PRIOR APPLICATION NUMBER: 60/206, 848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207, 727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230, 335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230, 347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242, 578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253, 625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257, 931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267, 636
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SEQ ID NO: 65277
 ; LENGTH: 336
 ; TYPE: PRT
 ; ORGANISM: *Neisseria gonorrhoeae*
 ; US-10-282-122A-65277
 Query Match 17.7%; Score 109.5; DB 12; Length 336;
 Best Local Similarity 30.0%; Pred. No. 0.0004; Indels 3; Gaps 3;
 Matches 27; Conservative 16; Mismatches 44; Indels 3; Gaps 3;
 RESULT 14
 ; Sequence 50897, Application US/1028212A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cherry
 ; APPLICANT: Hasebeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forstch, R.
 ; FILE REFERENCE: ELITRA.034A
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206, 848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207, 727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230, 335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230, 347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242, 578
 ; PRIOR FILING DATE: 2000-10-23
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 50897
 ; LENGTH: 348;
 Query Match 17.6%; Score 109; DB 12; Length 348;
 Best Local Similarity 29.7%; Pred. No. 0.00048; Mismatches 16; Indels 12; Gaps 27;
 Matches 27; Conservative 36; Mismatches 36;
 Qy 10 VTIATQDTERYACVSGESL-----AGMAKLGRGTRIPVGCLNGGCCVKYRVLGAVRKLG 6
 ; Sequence 50897, Application US/1028212A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J
 ; APPLICANT: Kovacic, David K
 ; APPLICANT: Zhou, Yihwei
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with Improvement of Plants and Use Thereof For Plant Improvement
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO: 275773
 ; LENGTH: 169
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Cline ID: PAT_MRT3847_91042C.1:pep
 ; US-10-424-599-275773
 Query Match 17.0%; Score 105.5; DB 12; Length 169;
 Best Local Similarity 40.0%; Pred. No. 0.0005; Mismatches 18; Indels 9; Gaps 24;
 Matches 24; Conservative 9; Mismatches 18;
 Qy 39 IPVGCLNGGCCVKYRVLGAVRK---LGPISRHVSAAEENDGYALACRVYDGVDELE 9
 ; Sequence 50897, Application US/1028212A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206, 848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207, 727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230, 335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230, 347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242, 578
 ; PRIOR FILING DATE: 2000-10-23

A;Title: Nucleotide sequence and functional analysis of the complete phenol/3,4-dimethyl Biochemistry 30, 1635-1641, 1991
 A;Reference number: S24417; MUID:9212108; PMID:1732207
 A;Accession: S24417
 A;Molecule type: DNA
 A;Residues: 1-108 <YOU>
 A;Cross-references: GB:ME60055; GB:J05317; NID:9151380; PIDN:AAA25898.1; PID:9151382
 A;Superfamily: chloroplast-type ferredoxins.
 A;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein
 A;Domain: 2Fe-2S; ferredoxin [2Fe-2S] homology <FER>
 A;Reference number: S16193; MUID:91293320; PMID:2065785
 A;Accession: S16368
 A;Molecule type: DNA
 A;Residues: 1-108 <IR>>
 A;Cross-references: GB:SA0145; NID:9311896; PIDN:CAA13701.1; PID:9311897
 C;Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology
 C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein
 F;40-81/Domain: ferridoxin [2Fe-2S] homology <FER>
 F;40-45,48-80/Binding site: 2Fe-2S cluster (cys) (covalent) #status predicted

Query Match Score 172.5; DB 1; Length 112;
 Best Local Similarity 41.0%; Pred. No. 6.1e-10;
 Matches 34; Conservative 16; Mismatches 32; Indels 1; Gaps

Qy 17 ERYACVSGESLILAGMAKLGRRGIPVGCCLNGCQVCKVRVLRGAVRKLGPISRRAHVSAAEE 76
 Db 15 QFRCLQDQSVLSAMEQQGRKRCVCPVGRGGCCGLCKVRVLSGTY-QCKHMSCNHVPEAA 73

Query Match Score 172.5; DB 1; Length 112;
 Best Local Similarity 41.0%; Pred. No. 6.1e-10;
 Matches 34; Conservative 16; Mismatches 32; Indels 1; Gaps

Qy 77 NDGYALACRVYPDGDYVLEAVGR 99
 Db 74 KQGLALACQLPQTIDNIECLRR 96

RESULT 5

Query Match Score 186; DB 1; Length 108;
 Best Local Similarity 42.6%; Pred. No. 2.8e-11;
 Matches 40; Conservative 12; Mismatches 38; Indels 4; Gaps 2;

Qy 10 VTIQQTDERYACVSGESLILAGMAKLGRRGIPVGCCLNGCQVCKVRVLRGAVRKLGPISRRA 69
 Db 7 ITVQPGGERFVQDQPSQALHANETQGGRCLIPVQCRGGCCGLCKVRVLAGDYES-GRYSKCK 65

Query Match Score 186; DB 1; Length 108;
 Best Local Similarity 42.6%; Pred. No. 2.8e-11;
 Matches 40; Conservative 12; Mismatches 38; Indels 4; Gaps 2;

Qy 70 HVSAEEENDGYALACRVYPDGDYVLEAVGRLRK 103
 Db 66 HLPVEAREQGYALACRIFARSCLIE--RYSKP 96

RESULT 3

T31266 ferredoxin [2Fe-2S]-like protein xylT - Spingomonas aromaticivorans plasmid pNL1
 C;Species: Spingomonas aromaticivorans
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
 C;Accession: T31266
 C;Cross-references: EMBL:X80765; NID:9527546.1; PIDN:CAA56746.1; PID:9527553
 R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, B.C.; Sansen, C.W.; C. Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
 R;Ng, L.C.; Shingler, V.; Sze, C.C.; Poh, C.L.
 A;Description: Complete sequence of a 184 kb catabolic plasmid from Spingomonas aromaticivorans
 A;Reference number: Z20992
 A;Accession: T31266
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-93 <ROM>
 A;Cross-references: EMBL:AF079317; NID:93378407; PIDN:AAD03990.1
 C;Genetics:
 A;Gene: xylT
 A;Genome: plasmid pNL1

Query Match Score 172.5; DB 2; Length 93;
 Best Local Similarity 44.3%; Pred. No. 5.1e-10;
 Matches 35; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

Qy 18 RIYACVSGESLILAGMAKLGRRGIPVGCCLNGCQVCKVRVLRGAVRKLGPISRRAHVSAAEE 77
 Db 15 QFACPEGERVLLAMERSGNDIGVCRGGSCGFVVRVVEGYR-TGRNSTAKVSVADQA 73

Query Match Score 166.5; DB 1; Length 101;
 Best Local Similarity 40.0%; Pred. No. 2.2e-09;
 Matches 34; Conservative 17; Mismatches 33; Indels 1; Gaps 1;

Qy 78 DGYALACRVYPDGDYVLE 96
 Db 74 KGYVLAACRVXPFLNDVTEI 92

Query Match Score 166.5; DB 1; Length 101;
 Best Local Similarity 40.0%; Pred. No. 2.2e-09;
 Matches 34; Conservative 17; Mismatches 33; Indels 1; Gaps 1;

Qy 17 ERYACVSGBLLAGMAKLGRRGIPVGCCLNGCQVCKVRVLRGAVRKLGPISRRAHVSAAEE 76
 Db 15 QSFTRPQDSVLRAMEEQKRCVPGCRGGCCGLCKVRVLSGDX-QCKHMSCNHVPEAA 73

Query Match Score 166.5; DB 1; Length 101;
 Best Local Similarity 40.0%; Pred. No. 2.2e-09;
 Matches 34; Conservative 17; Mismatches 33; Indels 1; Gaps 1;

Qy 77 NDGYALACRVYPDGDYVLEAVGR 101
 Db 74 QQGLALACQDLYRADLYIESLRQVR 98

RESULT 4

S24417 ferredoxin [2Fe-2S]-like protein dmpQ - Pseudomonas putida
 C;Species: Pseudomonas putida
 C;Accession: S24417
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 J. Bacteriol. 174, 711-724, 1992

T46585
 Ferredoxin reductase [imported] - *Pseudomonas stutzeri*
 C;Species: *Pseudomonas stutzeri*
 C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 11-May-2000
 C;Accession: T46585
 R;OuchiYama, N.; Miyachi, S.; Omori, T.
 J;Gen. Appl. Microbiol. 44, 57-63, 1998
 A;Title: Cloning and nucleotide sequence of carbazole catabolic genes from *Pseudomonas*
 A;Reference number: Z23091
 A;Accession: T46585
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-337 <KUR>
 A;Cross-references: EMBL:AB001723; PIDN:BA31273.1
 A;Experimental source: strain OM1
 C;Function:
 A;Description: involved in carbazole degradation [validated, PIR:Z23091]
 C;Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolog
 Query Match 20.9%; Score 129.5; DB 2; Length 329;
 Best Local Similarity 39.0%; Pred. No. 2.9e-05;
 Matches 30; Conservative 11; Mismatches 35; Indels 1; Gaps 1;
 Qy 21 CVSGESLLAGMAKLRGGTIPVGCLNNGGCCYCKVRLGAVRKLGPISSRAEEENDCY 80
 Db 14 CGSKSLIVSALANG-IGFPYECASGGCGVCKFELLEGNVQSMWPDAPGLSSREREKGR 72
 Qy 81 ALACRVPDPGDELEVA 97
 Db 73 HLACQCVVALSDLRIKVA 89

RESULT 7
 T31263
 xylylene monooxygenase (EC 1.14.1.1) chain A - *Sphingomonas aromaticivorans* plasmid pNL1
 C;Species: *Sphingomonas aromaticivorans*
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C;Accession: T31263
 R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G
 submitted to the EMBL Data Library, July 1998
 A;Description: Complete sequence of a 184 kb catabolic plasmid from *Sphingomonas aromatic*
 A;Reference number: 220992
 A;Accession: T31263
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-346 <ROM>
 A;Cross-references: EMBL:AF079317; NID:93378261; PIDN:AAD03987.1
 A;Gene: xyla
 A;Genome: Plasmid pNL1
 C;Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolog
 C;Keywords: oxidoreductase

Query Match 19.9%; Score 123; DB 2; Length 346;
 Best Local Similarity 30.1%; Pred. No. 0.00013;
 Matches 31; Conservative 20; Mismatches 46; Indels 6; Gaps 3;

Qy 9 TVTIQATQDERYACYSGESLLAGMAKLRGGTIPVGCLNNGGCCYCKVRLGAVRKLGPISS 68
 Db 12 TVTVEGSP7LTD1PAGKTLLEAMLDAG-LAMPHDCKVSGCGTICKFKLVSGKIGELSSAL 70
 Qy 69 AHVSAEEENDGYALACRVPPDGVDELEVA GRDRKPFEGGMAA 111
 Db 71 A-LEGDELRSGFRLACQAIPRSULTIAVA---PLSQGIAA 108

RESULT 8
 A12723
 naphthalene 1,2-dioxygenase [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C;Accession: A12723
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J

erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: A12723
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-337 <KUR>
 A;Cross-references: GB:AE008688; PIDN:AAL42207.1; PID:917739599; GSPDB:GN00186
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:

C;Gene: Atul196
 A;Map position: circular chromosome
 C;Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolog
 C;Keywords: 2Fe-2S metalloprotein
 F;40,45,48,80/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 18.4%; Score 114; DB 2; Length 337;
 Best Local Similarity 33.3%; Pred. No. 0.00098;
 Matches 31; Conservative 13; Mismatches 33; Indels 16; Gaps 4;
 Qy 9 TVTIQATQDERYACYSGESL---AGMAKLRGGTIPVGCLNNGGCCYCKVRLGAV-R 61
 Db 7 TIVLPQGRSMAEGTIVLQAAAGIA-----YPRGCRMGRGACKSHLISGBIDLL 60
 Qy 62 KLGPISRHVAEAEENDGYALACRVPPDGVEL 94
 Db 61 KHTPFS--LTEEEKAEGTLACRAVAPASDVTI 90

RESULT 9
 E97505
 phenol hydroxylase component, poxF (AF026065) [imported] - *Agrobacterium tumefaciens* (strain C58)
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C;Accession: E97505
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, R.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2326-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* C58
 A;Reference number: A97359; MUID:21608551; PMID:11743194
 A;Accession: E97505
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-337 <KUR>
 A;Cross-references: GB:AE007869; PIDN:AAK86998.1; PID:915156240; GSPDB:GN00169
 C;Genetics:
 A;Gene: AGR_C_2205
 A;Map position: circular chromosome
 C;Superfamily: methane monooxygenase reductase component; cytochrome-b5 reductase homolog
 C;Keywords: 2Fe-2S metalloprotein
 F;40,45,48,80/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 18.4%; Score 114; DB 2; Length 337;
 Best Local Similarity 33.3%; Pred. No. 0.00098;
 Matches 31; Conservative 13; Mismatches 33; Indels 16; Gaps 4;
 Qy 9 TVTIQATQDERYACYSGESL---AGMAKLRGGTIPVGCLNNGGCCYCKVRLGAV-R 61
 Db 7 TIVLPQGRSMAEGTIVLQAAAGIA-----YPRGCRMGRGACKSHLISGBIDLL 60
 Qy 62 KLGPISRHVAEAEENDGYALACRVPPDGVEL 94
 Db 61 KHTPFS--LTEEEKAEGTLACRAVAPASDVTI 90

RESULT 10
 GB2970
 probable ferredoxin PA5411 [imported] - *Pseudomonas aeruginosa* (strain PAO1)
 C;Species: *Pseudomonas aeruginosa*

Query Match 17.0%; Score 105; DB 2; Length 350;
 Best Local Similarity 28.4%; Pred. No. 0.0078; 18; Mismatches 43; Indels 2; Gaps 2;
 Matches 25; Conservative 18; Mismatches 43; Indels 2; Gaps 2;
 Query 9 TTVIAQTDERYACVSGESLLAMAKLGRGIVGCLNGGCCVYKVRKLGAVRKLGPISR 68
 Db 19 TSVVRGQGFQFQVPRGOTILESALAHQ-IAPFHDKVSGCGRKYLISGRVNE-TSSA 76
 Query 9 AHVSAEPEndGyALACRVPDGELEY 96
 Db 77 MGJSGDLYQSGYRGLGCQPKEDLEIEL 104

RESULT 14

A47016 toluene-4-monoxygenase (EC 1.12.1.1) reductase component - Pseudomonas mendocina
 C;Species: Pseudomonas mendocina
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A47016
 R;Yen, K.M.; Karl, M.R.
 J;Bacteriol. 174, 7253-7261, 1992
 A;Title: Identification of a new gene, tmof, in the Pseudomonas mendocina KRI gene cluster
 A;Reference number: A47016; MUID:93054339; PMID:1429451
 A;Accession: A47016
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-326 <YEN>
 A;Cross-references: GB:M95045; NID:9151596; PIDN:AAA6004.1; PID:9151597
 A;Note: sequence extracted from NCBI backbone (NCBIN:118027, NCBIP:118029)

C;Gene: tmof
 C;Superfamily: methane monooxygenase reductase component: cytochrome-b5 reductase homolog
 C;Keywords: 2Fe-2S; flavoprotein; iron-sulfur protein; metalloprotein; oxidoreductase
 F;107-77:Domain: ferredoxin [2Fe-2S] homology <FR>
 F;107-320/Domain: cytochrome-b5 reductase homology <CBR>
 F;36, 41, 44, 76/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 16.9%; Score 104.5; DB 1; Length 326;
 Best Local Similarity 31.5%; Pred. No. 0.0082; 16; Mismatches 40; Indels 5; Gaps 3;
 Matches 28; Conservative 16; Mismatches 40; Indels 5; Gaps 3;

Query 14 QTDE--RYACVSGESLLAMAKLGRGIVGCLNGGCCVYKVRKLGAVRKLGPISRH 70
 Db 5 QSDLLLHFEADSNLTLUSA-ALRAELVFPYCNSSGCCACKELIEEVSNLMP-DARG 62
 Query 71 VSAEPEndGyALACRVPDGELEYAGR 99
 Db 63 LAARELRRNRFLLACQCTPLSDLKIVN 91

RESULT 15

D81918 sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) chain F NMA0747 [similar]
 C;Species: Neisseria meningitidis
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C;Accession: D81918
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, H.; Hollroyd, S.; Jagels, K.; Leather, S.; Moulé, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A;Reference number: A811775; MUID:20222556; PMID:10761919
 A;Accession: D81918
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-405 <PAR>
 A;Cross-references: GB:AL162754; GB:AL157959; NID:97379424; PIDN:CAB84030.1; PID:g737946

A;Experimental source: serogroup A, strain Z2491
 C;Genetics:
 A;Gene: norF; NMA0747
 C;Species: methane monooxygenase reductase component; cytochrome-b5 reductase homolog
 C;Keywords: NAD; oxidoreductase

Search completed: August 5, 2004, 13:17:20
 Job time : 17 secs



SwissProt_42:*						
Database :	Score	Query	Match	Length	DB	ID
1	195.5	31.6	112	1	PERX	PSEPU
2	186	30.0	108	1	FERN	PSEPU
3	112	18.1	411	1	NORF	HAETN
4	105	17.0	350	1	XYL	PSEPU
5	104.5	16.9	326	1	TMOF	PSEME
6	104	16.8	405	1	NORF	NEIMA
7	104	16.8	405	1	NORF	NEIMB
8	100	16.6	348	1	MMOC	METCA
9	100	16.2	407	1	NORF	PASMU
10	99	16.0	408	1	NORF	VIBCH
11	98	15.8	352	1	DMBP	_PSBSP
12	98	15.8	407	1	NORF	VIBAL
13	96	15.5	407	1	NORF	VIBPA
14	96	15.5	407	1	NORF	VIBU
15	93	15.0	407	1	NORF	YERPE
16	92.5	14.9	301	1	NORF	SHRPNU
17	92	14.9	93	1	FERL	PERBI
18	91	14.7	104	1	FER2	SYNP6
19	90.5	14.6	95	1	FER	GLEJA
20	90.5	14.6	356	1	PAE	ECOLJ
21	90.5	14.6	431	1	HCR	CHLPN
22	90	14.5	407	1	NORF	VIBHA
23	89.5	14.5	96	1	FERL	PHYAM
24	89.5	14.5	96	1	FERL	PHYAM
25	89.5	14.5	303	1	NORF	COLMA
26	89.5	14.5	303	1	NORF	VIBPS
27	89.5	14.5	322	1	HCR	ECOLJ
28	88.5	14.3	431	1	NORF	CHLTR
29	88	14.2	328	1	NORF	PSEPU
30	87.5	14.1	348	1	BNC	ACICA
31	87	14.1	93	1	FER2	EQUTE
32	86.5	14.0	431	1	NORF	CHLNU
33	86	13.9	93	1	FER2	EQUAR

RESULT 1						
PERX_PSEPU		STANDARD		PRT;		
ID	PERX_PSEPU	PERX_PSEPU	STANDARD	PERX_PSEPU	STANDARD	PRT;
AC	P23103;					
DT	01-NOV-1991 (Rel. 20, Created)					
DT	01-NOV-1991 (Rel. 20, Last sequence update)					
DT	28-FEB-2003 (Rel. 41, Last annotation update)					
DE	Ferredoxin, plant-type.					
GN	XYLT.					
OS	Pseudomonas putida.					
OG	Plasmid TOL PWWO.					
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.					
OC	Pseudomonadaceae; Pseudomonas.					
OX	NCBI_TaxID:303;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=91293320; PubMed=2065785;					
RA	Harayama S., Polissi A., Reik M.;					
RT	"Divergent evolution of chloroplast-type ferredoxins."					
RL	FEBS Lett. 285:85-88(1991).					
CC	- - FUNCTION: Ferredoxins are iron-sulfur proteins that transfer electrons in a wide variety of metabolic reactions.					
CC	- - PATHWAY: Catechol metabolism.					
CC	- - SIMILARITY: Belongs to the 2Fe2S plant-type ferredoxin family.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce , or send an email to license@isb-sib.ch).					
CC	-----					
DR	EMBL; X61467; CAA43702.1; -					
DR	EMBL; M61747; AAA24051.1; -					
DR	PIR; S16193; S16193.					
DR	InterPro; IPR006050; 2Fe2S_fdb.					
DR	InterPro; IPR001041; Ferredoxin.					
DR	ProDom; PF00111; fer2; 1.					
DR	PROSITE; PS00197; 2Fe2S_FERREDOXIN_1.					
KW	Aromatic hydrocarbons catabolism; Electron transport; Metal-binding; Metal-sulfur; Iron; 2Fe-2S; Plasmid.					
FT	METAL 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).					
FT	METAL 4.6 IRON-SULFUR (2FE-2S) (BY SIMILARITY).					
FT	METAL 4.9 IRON-SULFUR (2FE-2S) (BY SIMILARITY).					
FT	METAL 9.1 IRON-SULFUR (2FE-2S) (BY SIMILARITY).					
SQ	SEQUENCE 112 AA; 12034 MW; 7994DFO33DF05D86 CRC64;					
Query Match	31.6%	Score 195.5;	DB 1;	Length 112;		
Best Local Similarity	48.1%	Pred. No. 8.1e-13;				
Matches 38;	Conservative 13;	Mismatches 27;	Indels 1;	Gaps		1;
Qy	17 ERVACVSGESLZAGMAKLGRGLRGPVGLCLNGGCVYCKVRLGAVRKLGPTISRHYSAEEB	76				
Db	15 QSPRCAEGOSVLRAMEAQKRCIPVGRGGCGJCERVLSGARYS-GRMSGRVPAKAKA	73				

QY	77	NDGYALACRYVPGDGVLE 95	RESULT 3	NQR HAEIN	STANDARD;	PRT;	411 AA.
Db	74	AEALALACQVFQTDLTI 92		ID "NQR HAEIN			
		:		AC 005012;			
		:		AC 16-OCT-2001 (Rel. 40, Created)			
		:		DT 16-OCT-2001 (Rel. 40, Last sequence update)			
		:		DT 28-FEB-2003 (Rel. 41, Last annotation update)			
		:		DE Na (+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.)			
		:		DE (Na (+)-translocating NQR subunit F) (Na (+)-NQR subunit F) (NQR complex subunit F) (NQR subunit F) (NQR OR HI0171)			
		:		DE subunit F) (NQR OR HI0171)			
		:		GN Haemophilus influenzae			
		:		OS Haemophilus influenzae			
		:		CC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
		:		OC Pasteurellaceae; Haemophilus.			
		:		NCBI_TaxID=727;			
		:		RN [1] -			
		:		RP SEQUENCE FROM N.A.			
		:		RC STRAIN=RD / KW20 / ATCC 51907;			
		:		RX MEDLINE=93350630; PubMed=1542800;			
		:		RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Heidelberg B., Utterback T.R., Phillips C.A., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geesey G.N., Smith H.O., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.; RT "Whole-genome random sequencing and assembly of Haemophilus influenzae [2]"			
		:		RT Science 269:496-512 (1995).			
		:		RN [2] -			
		:		RP IDENTIFICATION AS NQR SYSTEM.			
		:		RC STRAIN=RD / KW20 / ATCC 51907;			
		:		RX MEDLINE=96176316; PubMed=1601449;			
		:		RA Hayashi M., Nakayama Y., Unemoto T.; RT "Existence of Na+-translocating NADH-quinone reductase in Haemophilus influenzae,"			
		:		RT FEBS Lett. 381:174-176 (1996).			
		:		RL -!- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by nqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer pathway.			
		:		CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) + ubiquinol + Na(+) (Out).			
		:		CC -!- COFACTOR: FAD; a 2Fe-2S cluster (By similarity).			
		:		CC -!- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrE, nqrF (By similarity).			
		:		CC -!- SUBCELLULAR LOCATION: Inner membrane (Potential).			
		:		CC -!- SIMILARITY: Belongs to the nqrF family.			
		:		CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
		:		CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
		:		CC DR EMBL; X61466; CAN3701.1; -.			
		:		DR EMBL; M60055; AAA5898.1; -.			
		:		DR PTR; B39181; B39181.			
		:		DR InterPro; IPR006098; 2Fe2S_fAD_B5.			
		:		DR InterPro; IPR001041; Ferredoxin.			
		:		DR Pfam; PF00111; fer2_1.			
		:		DR PROSITE; PS00197; 2FE2S_FERREDOXIN_1.			
		:		DR KWR Iron-sulfur; Iron; 2Fe-2S; Plasmid; Electron transport; Metal-binding; Aromatic hydrocarbons catabolism; Electron transport; Metal-binding;			
		:		FT METAL 40 40 IRON-SULFUR (2FE-2S) (BY SIMILARITY)			
		:		FT METAL 45 45 IRON-SULFUR (2FE-2S) (BY SIMILARITY)			
		:		FT METAL 48 48 IRON-SULFUR (2FE-2S) (BY SIMILARITY)			
		:		FT METAL 80 80 IRON-SULFUR (2FE-2S) (BY SIMILARITY)			
SQ	SEQUENCE	108 AA;	11913 MW;	9FB8181EB361574E CRC64;			
				Query Match 30 0%; Score 186; DB 1; Length 108;			
				Best Local Similarity 42.6%; Pred. No. 7e-12; Mismatches 4; Gaps 2;			
				Matches 40; Conservative 12; Mi.matches 38;			
QY	10	VTIAQTDERYACVSGESILLAGMAKIGRRGIPVGCLNGGGVCKVRLGAVRKLGPIISRA 69	10	VTIAQTDERYACVSGESILLAGMAKIGRRGIPVGCLNGGGVCKVRLGAVRKLGPIISRA 69	10	ITVQPGSERVCPQPSAHLMETQKRCRIPVGCRGCGICKVRLGAVRKLGPIISRA 69	10
Db	7	ITVQPGSERVCPQPSAHLMETQKRCRIPVGCRGCGICKVRLGAVRKLGPIISRA 69	7	ITVQPGSERVCPQPSAHLMETQKRCRIPVGCRGCGICKVRLGAVRKLGPIISRA 69	7	ITVQPGSERVCPQPSAHLMETQKRCRIPVGCRGCGICKVRLGAVRKLGPIISRA 69	7
QY	70	HVSAAEENDGYALACRYVPGDGVLEAVGRILRK 103	70	HVSAAEENDGYALACRYVPGDGVLEAVGRILRK 103	70	HLPVREAQGYALACRFLARSIDLCTE--RYSKP 96	70
Db	66	HLPVREAQGYALACRFLARSIDLCTE--RYSKP 96	66	HLPVREAQGYALACRFLARSIDLCTE--RYSKP 96	66	InterPro; IPR001433; oxford_FAD/NAD (P).	66

SIMILARITY IN THE N-TERMINAL REGION WITH 2FE-2S FERREDOXINS, AND

IN THE REST OF THE SEQUENCE WITH FERREDOXIN REDUCTASE.

-1- SIMILARITY: TO OTHER BACTERIAL RING-HYDROXYLATING DIOXYGENASE - ELECTRON TRANSFER COMPONENTS.

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CC EMBL; M95045; AAA26004.1; -.

CC DR PIR; A47016; A47016.

CC DR InterPro; IPR006158; 2Fe2S fd BS.

CC DR InterPro; IPR008333; FAD binding_6.

CC DR InterPro; IPR001041; Ferredoxin.

CC DR InterPro; IPR001433; Oxred_FAD/NAD (P).

CC DR InterPro; IPR001221; Phe_hydroxylase.

CC DR Pfam; PF00970; FAD binding_6; 1.

CC DR Pfam; PF00111; fer2; 1.

CC DR Pfam; PF00175; NAD binding_1; 1.

CC DR PRINTS; PR00371; FPNCR.

CC DR PROSITE; PS00197; 2Fe2S_FERREDOXIN_1.

CC KW Aromatic hydrocarbons catabolism; Flavoprotein; FAD; NAD;

CC KW Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.

CC FT DOMAIN 25 94 FERREDOXIN.

CC FT DOMAIN 95 326 FERREDOXIN-REDUCTASE.

CC FT METAL 36 36 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

CC FT METAL 41 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

CC FT METAL 44 44 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

CC FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY).

CC SQ SEQUENCE 326 AA; 35983 MW; 1788.9D794FC092EE CRC64;

Query Match 16.9% Score 104.5; DB 1; Length 326;

Best Local Similarity 31.5%; Pred. No. 0.0029;

Matches 28; Conservative 16; Mismatches 40; Indels 5; Gaps 3;

QY 14 QTDE--RYACVSGESIILLAGMAKURRGIPVGCLNGGCCVCKYRVLRGAVRKLGPIISRAH 70

Db 5 QSDDILHFFEADSNTLLSA-ALPRLVELVPEYCNSGGCACKIELEGEVSNLWP-DAPG 62

QY 71 VSAAEENDGYALACKVPPDDEVELVAGR 99

Db 63 LAARRLKRNRFLACCQCKPLSDLKIKVNR 91

RESULT 6

NQRF NEIMA ID NORF NEIMA STANDARD; PRT; 405 AA.

AC Q9JUQ3; Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE NA (-)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)

DE (Na(+))-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex

DE subunit F) (NQR-1 subunit F).

GN NQRF OR NMA074*.

OS Neisseria meningitidis 'serogroup A'.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

NCBI_TaxID=65699;

[1]

RN SEQUENCE FROM N.A.

RC SEQUENCE=22491 / Serogroup A / Serotype 4A;

RC MEDLINE=20222556; PubMed=10761919;

RX Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

RA Jaeger K., Leather S., Moyle S., Simmonds M., Sungill K., Quail M.A.,

RA Palaniswami M.A., Rutherford K.M., Simmonds M., Skelton J.,

RA	Whitehead S., Spratt B.G., Barrell B.G./	Sequence of a serogroup A strain of <i>Neisseria meningitidis</i> 22491.1;
RT	"Complete DNA sequence of a serogroup A strain of <i>Neisseria meningitidis</i> 22491.1;"	Nature 404:502-506 (2000).
RL	"FUNCTION: NQR complex catalyzes the reduction of ubiquinol by two successive reactions, coupled with the reduction of Na(+) ions from the cytoplasm to the periplasm. The NQR complex is catalyzed by nqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubiquinone by a one-electron pathway (By similarity)."	NQR complex catalyzes the reduction of ubiquinol by two successive reactions, coupled with the reduction of Na(+) ions from the cytoplasm to the periplasm. The NQR complex is catalyzed by nqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubiquinone by a one-electron pathway (By similarity)."
CC	"CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD ubiquinol + Na(+) (Out)."	"CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD ubiquinol + Na(+) (Out)."
CC	"-1- COFACTOR: FAD and a 2Fe-2S cluster (By similarity)."	"-1- COFACTOR: FAD and a 2Fe-2S cluster (By similarity)."
CC	"-1- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD and nqrE (By similarity)."	"-1- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD and nqrE (By similarity)."
CC	"-1- SUBCELLULAR LOCATION: Inner membrane (Potential)."	"-1- SUBCELLULAR LOCATION: Inner membrane (Potential)."
CC	"-1- SIMILARITY: Belongs to the nqrF family."	"-1- SIMILARITY: Belongs to the nqrF family."
CC	"This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is not modified and this statement is not removed. Usage by and/or modification of this statement is not allowed. Usage of this entry in modified software requires a license agreement (see http://www.isb-sib.ch or send an email to license@isb-sib.ch)."	"This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is not modified and this statement is not removed. Usage by and/or modification of this statement is not allowed. Usage of this entry in modified software requires a license agreement (see http://www.isb-sib.ch or send an email to license@isb-sib.ch)."
CC	"EMBL: AL162754; CAB84030.1; -."	"EMBL: AL162754; CAB84030.1; -."
CC	"DR PIR: DB1918; DB1918."	"DR PIR: DB1918; DB1918."
CC	"DR HSPP: P23486; 1QDQ."	"DR HSPP: P23486; 1QDQ."
CC	"DR HAMAP: MF_00430; -; 1."	"DR HAMAP: MF_00430; -; 1."
CC	"DR InterPro; IPR006058; 2Fe2S_fld_BS."	"DR InterPro; IPR006058; 2Fe2S_fld_BS."
CC	"DR InterPro; IPR008333; FAD_binding_6."	"DR InterPro; IPR008333; FAD_binding_6."
CC	"DR InterPro; IPR001041; Ferredoxin."	"DR InterPro; IPR001041; Ferredoxin."
CC	"DR InterPro; IPR001709; FPN_cyt_redctse."	"DR InterPro; IPR001709; FPN_cyt_redctse."
CC	"DR InterPro; IPR001433; Oxred_FAD/NAD (P)."	"DR InterPro; IPR001433; Oxred_FAD/NAD (P)."
CC	"DR Pfam: PF00970; FAD_binding_6; 1."	"DR Pfam: PF00970; FAD_binding_6; 1."
CC	"DR Pfam: PF00111; fer2; 1."	"DR Pfam: PF00111; fer2; 1."
CC	"DR Pfam: PF00175; NAD_binding_1; 1."	"DR Pfam: PF00175; NAD_binding_1; 1."
CC	"DR PRINTS: PR00371; FPNCR."	"DR PRINTS: PR00371; FPNCR."
CC	"DR PROSITE; PS00197; 2Fe2S_FERREDOXIN; FALSE NEG."	"DR PROSITE; PS00197; 2Fe2S_FERREDOXIN; FALSE NEG."
KW	"Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S Transmembrane; Inner membrane; Complete proteome."	"Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S Transmembrane; Inner membrane; Complete proteome."
FT	"FT TRANSMEM 2 24 FERREDOXIN."	"FT TRANSMEM 2 24 FERREDOXIN."
FT	"FT DOMAIN 34 114 FERREDOXIN."	"FT DOMAIN 34 114 FERREDOXIN."
FT	"FT DOMAIN 270 387 CATALYTIC."	"FT DOMAIN 270 387 CATALYTIC."
FT	"FT METAL 67 67 IRON-SULFUR (2FE-2S) (BY SIMILARITY)"	"FT METAL 67 67 IRON-SULFUR (2FE-2S) (BY SIMILARITY)"
FT	"FT METAL 73 73 IRON-SULFUR (2FE-2S) (BY SIMILARITY)"	"FT METAL 73 73 IRON-SULFUR (2FE-2S) (BY SIMILARITY)"
FT	"FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY)"	"FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY)"
FT	"FT METAL 108 108 IRON-SULFUR (2FE-2S) (BY SIMILARITY)"	"FT METAL 108 108 IRON-SULFUR (2FE-2S) (BY SIMILARITY)"
SQ	"SQ SEQUENCE 405 AA; 45165 MW; E22DC9CF7B52B0A CRC64;"	"SQ SEQUENCE 405 AA; 45165 MW; E22DC9CF7B52B0A CRC64;"
QY	"Query Match 16.8%; Score 104; DB 1; Length 405; Best Local Similarity 35.2%; Pred. No. 0.004; Mismatches 32; Conservative 14; Mismatches 41; Indels 8 GTVIAQTDERYACV-SGESSILLAGMAKLGRGIPVGCLN63-CGVCKVRY"	"Query Match 16.8%; Score 104; DB 1; Length 405; Best Local Similarity 35.2%; Pred. No. 0.004; Mismatches 32; Conservative 14; Mismatches 41; Indels 8 GTVIAQTDERYACV-SGESSILLAGMAKLGRGIPVGCLN63-CGVCKVRY"
Qy	"66 ISRAHVAEEENDGYALACRYPDPDDELYEV 96	"66 ISRAHVAEEENDGYALACRYPDPDDELYEV 96
Db	"90 TELTSISKRAAREGCRLSQVNKTDMDIEV 120	"90 TELTSISKRAAREGCRLSQVNKTDMDIEV 120
DE	"Na (+)-translocating NADH-quinone reductase subunit F (EC 1.16.99.1)"	"Na (+)-translocating NADH-quinone reductase subunit F (EC 1.16.99.1)"

DE (Na(+)-translocating NQR subunit E) (Na(+)-NQR subunit F) (NQR complex
DE subunit F) (NQR-1 subunit F).
GN NQR OR NMB0564.
OS Neisseria meningitidis (serogroup B).
OC Bacterium; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=M058 / Serogroup B;
MEDLINE=20175/55; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., DeBoy R., Peterson J.D., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
RA Cottrell M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Ventur J.C.,
RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain
MC58.";
RT Science 287:1809-1815(2000).
CC -!- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to
ubiquinol by two successive reactions, coupled with the transport
of Na(+) ions from the cytoplasm to the periplasm. The first step
is catalyzed by nqrP, which accepts electrons from NADH and
reduces ubiquinone-1 to ubiquinol by a one-electron transfer
pathway (By similarity).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD (+) +
ubiquinol + Na(+) (Out).
CC -!- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
CC -!- SUBUNIT: Composed of six subunits: nqrA, nqrB, nqrC, nqrE
and nqrF (By similarity).
CC -!- SUBCELLULAR LOCATION: Inner membrane (Potential).
CC -!- SIMILARITY: Belongs to the nqrF family.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL; AE002412; AAFA0392.1; -
DR PIR; G81184; G81184.
DR HSSP; P23486; 1QFU.
DR TIGR; NMB0564; -.
DR HAMAP; MF_00430; -.
DR InterPro; IPR01041; Ferredoxin_1.
DR InterPro; IPR008333; 2Fe2S_fld_B6.
DR InterPro; IPR01433; Oxred_FAD/NAD(P).
DR Pfam; PF00970; FAD_binding_6_1.
DR Pfam; PF00111; fer2_1.
DR Pfam; PF00175; NAD_binding_1_1.
DR PROSITE; PS00197; 2Fe2S_FERREDOXIN; FALSE NEG.
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
KW Transmembrane; Inner membrane; Complete proteome.
FT DOMAIN 34 24 POTENTIAL.
FT DOMAIN 24 CATALYTIC.
FT DOMAIN 34 114 FERREDOXIN.
FT 270 387 IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
FT METAL 67 67 IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
FT METAL 73 73 IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
FT METAL 76 76 IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
FT METAL 108 108 IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
SQ SEQUENCE 405 AA; 45164 MW; 0F93B48FFC2AFCC CRC64;

QY 8 GTVTIAQTDERYACV-SGESLLAGMAKLRGIPVGCLNGG-CGYCKVRLGAVRKLG 65
Db 32 GDITKVNKGKEKLTMPAGGKILGALANEQ-IFIPSACGGGSGGQCRVVVKSGGDL-P 89
QY 66 ISRRAVSAEPEPDGYALACRVVPDGVLEV 96
Db 90 TELSHISKREAREGRLSCQVNKTMDIEV 120
RESULT 8
MMOC_METCA STANDARD; PRT; 348 AA.
ID MMOC_METCA
AC P2268;
DT 01-AUG-1991 (Rel. 19, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DB Methane monooxygenase component C (EC 1.14.13.25) (Methane
hydroxylase) (Methane monooxygenase reductase) (MMOR).
GN MMOC.
OS Methyllococcus capsulatus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Methyllococcales;
OC Methyllococcaceae; Methyllococcus.
OX NCBI_TAXID=414;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-16.
RC STRAIN=Bath;
RX Pubmed=220538;
RA Stainthorpe A.C., Lees V., Salmon G.P.C., Dalton H., Murrell J.C.;
RT "The methane monooxygenase gene cluster of *Methyllococcus capsulatus*
(Bath)." ;
RL Gene 91:27-34 (1990).
RN [2]
RP REVISION TO 254.
RA McDonald I., Murrell J.C.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP STRUCTURE BY NMR.
RC STRAIN=Bath;
RX Pubmed=2163398; Pubmed=11772001;
RA Mueller J., Lugovskoy A.A., Wagner G., Lippard S.J.;
RT "NMR structure of the [2Fe-2S] ferredoxin domain from soluble methane
monooxygenase reductase and interaction with its hydroxylase." ;
RL Biochemistry 41:42-51(2002).
CC -!- FUNCTION: Responsible for the initial oxygenation of methane to
methanol in methanotrophs. It also catalyzes the monohydroxylation
of a variety of unactivated alkenes, alicyclic, aromatic and
heterocyclic compounds. The component C is the iron-sulfur
flavoprotein of SMMO.
CC -!- CATALYTIC ACTIVITY: Methane + NAD(P)H + O(2) = methanol +
NAD(P) (+) + H(2)O.
CC -!- COFACTOR: Binds 1 2Fe-2S cluster.
CC -!- SUBUNIT: The soluble methane monooxygenase (SMMO) consists of four
components A/MMOH (composed of alpha/mmoX, beta/mmoY and
gamma/mmoZ), B/MMOB (mmoB), C/MMOR (mmoC) and D/MMOD (mmoD).
CC -!- SIMILARITY: In the N-terminal section; belongs to the 2Fe2S plant-
type ferredoxin family.
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or send an email to license@isb-sib.ch).
CC EMBL; M9050; AAB62391; -.
DR PDB; 1JQ4; 09-JAN-02.
DR InterPro; IPR006058; 2Fe2S_fld_BS.
DR InterPro; IPR01834; Cyt_B5 reductase.
DR InterPro; IPR008333; FAD_binding_6.
DR InterPro; IPR01041; Ferredoxin.
DR InterPro; IPR01709; FPN_cyt_reductase.
DR InterPro; IPR001433; Oxford_FAD/NAD(P).
DR InterPro; IPR00132; Conservative_14; Mismatches 41; Indels 4; Gaps 4;

RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
 RL Nature 406:477-483(2000).

-!- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by nqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubiquinol by a one-electron transfer pathway.
 CC CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) + ubiquinol + Na(+) (Out).
 CC -!- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).
 CC -!- SUBUNIT: Composed of six subunits: nqrA, nqrB, nqrC, nqrD, nqrE and nqrF (By similarity).
 CC -!- SUBCELLULAR LOCATION: Inner membrane (Potential).
 CC -!- SIMILARITY: Belongs to the nqrF family.

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 CC -----
 DR EMBL; AEL1731; ADD29967.1; .
 DR EMBL; AEL04300; AFR95434.1; .
 DR PIR; B12094; B82094.
 DR HSSP; P333007; 1BXR.
 DR TIGR; VC2290; .
 DR HAMAP; MF_00430; .
 DR InterPro; IPR006058; 2Fe2S_fad_BS.
 DR InterPro; IPR00833; FAD_binding_6.
 DR InterPro; IPR00104; Ferredoxin.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00175; fer2; 1.
 DR Pfam; PF00111; fer2; 1.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN; FALSE NEG.
 DR Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
 KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
 KW Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 5 24 POTENTIAL.
 DOMAIN 35 117 FERREDOXIN.
 FT DOMAIN 273 390 CATALYTIC.

FT METAL 70 70 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 79 79 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 111 111 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 SQ SEQUENCE 408 AA; 45066 MW; F5665E962/CAADB/CRC64;
 FT 16.0% Score: 99; DB: 1; Length: 408;
 Best Local Similarity 34.4%; Pred. No. 0.013;
 Matches 32; Conservative 14; Mismatches 41; Indels 6; Gaps 5;

8 GTVTIA-QTDERYACVS--GESULLAGMALKLGRGIPVGCLNGG-CGCVCKVRVLRGAVRK 63
 DB 33 GDTITDINGDPPEKAVTQPGKGLTALAGAG--VFVSSAACGGGSCQCRVKKSGGGDIL 91
 QY 64 GPISRAHVSAEEENDGYALCRVVPDCDVLEV 96
 DB 92 -PTELDHISKGFAREGERLACQAVAKADMIEU 123

RESULT 11
 DMPP_PSESP ID_P19734; STANDARD; PRT; 352 AA.
 AC AC

17; Created
 01-FEB-1991 (Rel.)
 01-FEB-1991 (Rel.)
 17; Last annotation update
 15-MAR-2004 (Rel.)
 43; Last annotation update
 DE Phenol hydroxylase P5 protein (EC 1.14.13.7) (Phenol 2-monoxygenase

DE PS component).
 GN DMP_P.
 OS Pseudomonas sp. (strain CF600).
 OC Plasmid pVR150.
 OC Bacteria; Proteobacteria.
 OX NCBI TaxID=306;
 RN [1] _TAXID=306;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9107231; PubMed=2254259;
 RA Powlowski J.; Shingler V.;
 RT "Complete nucleotide sequence and polypeptide analysis of multicomponent phenol hydroxylase from Pseudomonas sp. strain CF600."
 RT CF600.;
 RL J. Bacteriol. 172:6826-6833(1990).
 RN [2] _
 RP PROBABLE FUNCTION, AND SEQUENCE OF 1-4.
 RX MEDLINE=9107231; PubMed=2254259;
 RA Powlowski J.; Shingler V.;
 RT "In vitro analysis of polypeptide requirements of multicomponent phenol hydroxylase from Pseudomonas sp. strain CF600."
 RT J. Bacteriol. 172:6834-6840(1990).
 CC -!- FUNCTION: Catalyzes phenol, and some of its methylated derivatives. P5 is required for growth on phenol, and for in vitro phenol hydroxylase activity.
 CC -!- FUNCTION: Probable electron transfer from NADPH, via FAD and the 2Fe-2S center, to the oxygenase activity site of the enzyme.
 CC -!- CATALYTIC ACTIVITY: Phenol + NADP(+) + catechol + O(2) = catechol + O(2) + H(2)O.
 CC -!- COPARTNER: P5 contains a FAD cofactor and a ferredoxin-type 2Fe-2S cluster.
 CC -!- PATHWAY: Phenol biodegradation; first step.
 CC -!- SUBUNIT: The multicomponent enzyme phenol hydroxylase is formed by P0, P1, P2, P3, P4 and P5 polypeptides.
 CC -!- SIMILARITY: In the N-terminal section, belongs to the 2Fe2S plant-type ferredoxin Family.
 CC -----
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 CC -----
 DR M60276; AA25944.1; .
 DR HSSP; P00235; IFRR.
 DR InterPro; IPR006058; 2Fe2S_fad_BS.
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR003333; FAD_binding_6.
 DR InterPro; IPR001041; Ferredoxin.
 DR InterPro; IPR001221; Phe_hydroxylase.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00111; fer2; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PRINTS; PR00406; CYTB5RDNASE.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN.
 DR Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase;
 KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
 KW Electron transport; Plasmid.
 DR INIT MET 0 0
 FT METAL 36 36 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 41 41 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 44 44 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 FT METAL 76 76 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 38346 MW; 1E837F6A3E12E4 CRC64;

Query Match Score 98; DB 1; Length 352;
 Best Local Similarity 31.4%; Pred. No. 0.014;
 Matches 27; Conservative 15; Mismatches 42; Indels 2; Gaps 2;
 DE 10 VTIAGTDERYACVSGESLISLAGMAKLRRGGIPVGCLNGG-CGCVCKVRVLRGAVRK 69

RESULT 12			
		QRF_VIBAL	
b	4	VTEIPGEVIEWEDGQTILQAALRQG-VWLPPACGHGTCATCKVQVVEGEV-DIGEASPF	61
b	70	HVSAAEBENDGXALACRVPDGVLE 95	
b	62	ALMDIERDKVLLACCAPLSIVIE 87	
		STANDARD;	PRT;
b	5	NQRF_VIBAL	407 AA.
b	6	0565BA;	
b	7	16-OCT-2001 (Rel. 40, Created)	
b	8	16-OCT-2001 (Rel. 40, Last sequence update)	
b	9	28-FEB-2003 (Rel. 41, Last annotation update)	
b	10	Na (+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)	
b	11	(Na (+)-translocating NADH-quinone reductase subunit beta) (Na (-)-translocating NQR subunit F) (Na (+)-NQR subunit F) (NQR complex subunit F) (NQR-1 subunit F).	
b	12	Na (+)-NQR subunit F.	
b	13	NQRF_QB	
b	14	NQRF_QB	

Db	91 -PTELDHITKGEAREGERLACQVAMKTDMDIEL	1.22
RESULT 13		
NQR_VIBPA	STANDARD ;	PRT ; 407 AA.
ID	NORE_VIBPA	
Q9LJ0;		
AC	16-OCT-2001 (Rel. 40, Created)	
DT	10-OCT-2003 (Rel. 42, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
NA (+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)		
DE	(Na(+)-translocating NQR subunit F) (Na(+)-NQR subunit F) (NQR complex subunit F) (NQR-1 subunit F) .	
DE	NQR6 OR VP346.	
OS	Vibrio parahaemolyticus.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrioales;	
OC	Vibrionales; Vibrionaceae; Vibrionaceae; Vibrio.	
OX	NCBI_TaxID=670;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	SPBRAIN=LRMD_2210633 / Serotype O3:K6;	
RX	MEDLINE=22508454; PubMed=12620739;	
RA	Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iiima Y., Naijima M., Kuroba Y., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shingawa H., Hattori M., Iida T.; "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.", Lancet 361:743-749 (2003).	
RL	[2]	
RP	SEQUENCE OF 72-374 FROM N.A.	
RC	SPBRAIN=FCM_2147; PubMed=10779868;	
RX	MEDLINE=20441140; PubMed=10779868;	
RA	Kato S., Yumoto I., "Detection of the Na (+)-translocating NADH-quinone reductase in marine bacteria using a PCR technique.", Can. J. Microbiol. 46:325-332 (2000).	
RT	"Detection of the Na (+)-translocating NADH-quinone reductase in marine bacteria using a PCR technique."	
RL	Na (+)-FUNCTION: NQR complex catalyze the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by nqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer pathway.	
CC	-!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na (+) (In) = NAD (+) + ubiquinol + Na (+) (Out).	
CC	-!- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).	
CC	-!- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE and nqrF (By similarity).	
CC	-!- SUBCELLULAR LOCATION: Inner membrane (Potential).	
CC	-!- SIMILARITY: Belongs to the nqrF family.	
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CC	DR AP005081; BAC6069.1; -.	
EMBL; AB024725; BAA83762.1;		
DR HAMAP; MF_00430; -; 1.		
DR IPR006058; IPR00833; 2Fe2S fd BS.		
InterPro; IPR00833; FAD binding_.		
InterPro; IPR001041; Ferritin.		
DR InterPro; IPR001041; Ferritin.		
DR InterPro; IPR001179; FPN_cyt_reductse.		
DR InterPro; IPR001433; Oxred_FAD/NAD(P).		
DR Pfam; PF00111; fer2; 1.		
DR Pfam; PF00115; NAD binding_1; 1.		
DR PRINTS; PR03371; FPNCR.		
DR PROSITE; PS00197; 2Fe2S_FERRDOXIN.		
KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport; Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;		
KW	Transmembrane, Inner membrane; Complete proteome.	
FT	TRANSMEM 3 23	POTENTIAL.
FT	DOMAIN 34 116	FERRDOXIN.
FT	DOMAIN 272 389	CATALYTIC.
FT	METAL 69 69	IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
FT	METAL 75 75	IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
FT	METAL 78 78	IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
FT	METAL 110 110	IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
FT	CONFFLICT 114 114	V -> M (IN REF 2).
FT	CONFFLICT 185 185	Q -> E (IN REF 2).
FT	CONFFLICT 278 278	I -> V (IN REF 2).
FT	CONFFLICT 324 326	GLA -> MLO (IN REF 2).
SQ	SEQUENCE 407 AA; 45083 MW;	74DCC8E99EDBE3A CRC64;
Query Match	15.5%	Score: 96; DB 1; Length 407;
Best Local Similarity	31.28;	Pred. No. 0.025;
Matches	29;	Conservative 16; Mis matches 42; Indels 6; Gaps 4;
QY	8 GTYTA--QTDERYACSGESLLAGMAKLGRGRCIPVGCLNGG-CGVCKVVRGAVRKL 63	
Db	32 GDIRTISVNGSDADKAVTQPQGKLUISALAGAG-VEVSSAGGGGSGQCRVKVRSGGDTL 90	
QY	64 GPISRAHYSAAEENDGYALACRVPDGVLEV 96	
Db	91 -PTEDHITKGEAREGERLACQYAVKTMDIEL 122	
RESULT 14		
NQR_VIBVU		
ID	NQR_VIBVU	
AC	Q8BQJ1;	
DT	10-OCT-2003 (Rel. 42, Created)	
DT	10-OCT-2003 (Rel. 42, Last sequence update)	
DE	Na (+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)	
DE	(Na (+)-NQR subunit F) (NQR complex subunit F) (NQR-1 subunit F).	
GN	NQRF OR VV1826.	
OS	Vibrio vulnificus.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrio.	
OX	Vibrionaceae; Vibrio.	
NCBI_TaxID=672;		
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=FCM_2147;	
RX	MEDLINE=20441140; PubMed=10779868;	
RA	Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.; "Complete genome sequence of <i>Vibrio vulnificus</i> CMCP6."	
RT	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.	
CC	-!- FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions, coupled with the transport of Na(+) ions from the cytoplasm to the periplasm. The first step is catalyzed by nqrF, which accepts electrons from NADH and reduces ubiquinone-1 to ubisemiquinone by a one-electron transfer pathway (By similarity).	
CC	-!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na (+) (In) = NAD (+) + ubiquinol + Na (+) (Out).	
CC	-!- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).	
CC	-!- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE and nqrF (By similarity).	
CC	-!- SUBCELLULAR LOCATION: Inner membrane (Potential).	
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CC	DR AP005081; BAC6069.1; -.	
EMBL; AB024725; BAA83762.1;		
DR HAMAP; MF_00430; -; 1.		
DR IPR006058; IPR00833; 2Fe2S fd BS.		
InterPro; IPR00833; FAD binding_.		
DR InterPro; IPR001041; Ferritin.		
DR InterPro; IPR001179; FPN_cyt_reductse.		
DR InterPro; IPR001433; Oxred_FAD/NAD(P).		
DR Pfam; PF00111; fer2; 1.		
DR Pfam; PF00115; NAD binding_1; 1.		
DR PRINTS; PR03371; FPNCR.		
DR PROSITE; PS00197; 2Fe2S_FERRDOXIN.		
KW	Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport; Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;	
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	CC -!- SIMILARITY: Belongs to the nqrF family.	
CC	CC -!- COFACTOR: FAD and a 2Fe-2S cluster (By similarity).	
CC	CC -!- SUBUNIT: Composed of six subunits; nqrA, nqrB, nqrC, nqrD, nqrE and nqrF (By similarity).	
CC	CC -!- SUBCELLULAR LOCATION: Inner membrane (Potential).	
CC	CC -!- SIMILARITY: Belongs to the nqrF family.	
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DR InterPro: IPR006058; 2Fe2S fd BS.
 DR InterPro: IPR008333; FAD_binding_6.
 DR InterPro: IPR001041; Ferredoxin.
 DR InterPro: IPR001433; Oxred/FAD/NAD (P).
 DR Pfam: PF00970; FAD_binding_6_1.
 DR Pfam: PF00111; fer2_1.
 DR Pfam: PF00175; NAD_binding_1_1.
 DR PROSITE; PS00197; 2FE2S FERREDOXIN; FALSE NEG.
 KW Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
 KW Flavoprotein; FAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
 KW Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 5 24 Potential_1.
 FT METAL 69 69 IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
 FT METAL 75 75 IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
 FT METAL 78 78 IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
 FT METAL 110 110 IRON-SULFUR (2Fe-2S) (BY SIMILARITY).
 SQ SEQUENCE 407 AA; 44945 MW; 1FDEC95FF196715A2 CRC64;

Query Match 15.5%; Score 96; DB 1; Length 407;
 Best Local Similarity 31.2%; Pred. No. 0.025;
 Matches 29; Conservative 16; Mismatches 42; Indels 6; Gaps 4;

QY 8 GTVTIA- --QFDERYACVSGESLLAGMAKLGRRGIPVGCLINGG-CCTCKYVRLLGAVRK 63
 DB 32 GDTITNGDADKSVTSPGGKLLSALAGAG-VFVSSACGGGSCQCRVKVKGDDIL 90

QY 64 GPISRAHVSAAFFENDYALACRVPDQDVLFY 96
 DB 91 -PTELDHTIKGEAREGERLACQVAKTDDMTEL 122

RESULT 15
 NQRF_YERPE STANDARD; PRT; 407 AA.
 ID NQRF_YERPE
 AC Q8ZBZ5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Na (+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)
 DE (Na (+)-translocating NQR subunit F) (Na (+)-NQR subunit F) (NQR complex
 subunit F) (NQR-1 subunit F).
 CN NQRF OR YP03235 OR Y0956.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TAXID-632;
 RN SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; Pubmed=1586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebainia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks R., Cerdano-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C., Quail M.A., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague.";
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; Pubmed=12142410;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liiss P.,
 RA Ferreira N.T., Rose D.J., Mai B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Pano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of *Yersinia pestis* KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 CC -; FUNCTION: NQR complex catalyzes the reduction of ubiquinone-1 to
 CC ubiquinol by two successive reactions, coupled with the transport
 CC of Na(+) ions from the cytoplasm to the periplasm. The first step

Db	RESULT 2	Q9RB86	PRELIMINARY;	PRT;	113 AA.
	AC	Q9RB86;			
	DT	01-MAY-2000 (TREMBLrel. 13; Created)			
	DT	01-MAY-2000 (TREMBLrel. 13; Last sequence update)			
	DT	01-OCT-2003 (TREMBLrel. 25; Last annotation update)			
	DE	Chloroplast-type ferredoxin.			
	GN	PHNT2.			
	OS	Burkholderia sp. RP007.			
	OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;			
	OC	Burkholderiaceae; Burkholderia.			
	OX	NCBI_TAXID:83784;			
	RN	[1] _			
	RP	SEQUENCE FROM N.A.			
	RC	STRAIN:RP007;			
	RX	Medline=99382283; PubMed=10448110;			
	RA	Laurie A.D.; Lloyd-Jones G.;			
	RT	Conserved and hybrid meta-cleavage operons from PAH-degrading Burkholderia RP007.			
	RT	Biochem. Biophys. Res. Commun. 262:308-314(1999).			
	RL	CC -; COFACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).			
	DR	EMBL: AF112137; AAF02429.1; -.			
	DR	GO:0005489; P:electron transporter activity; IEA.			
	DR	GO:0006118; P:electron transport; IEA.			
	DR	InterPro: IPR006058; 2FE2S fd BS.			
	DR	InterPro; IPR01041; Perredoxin.			
	DR	Pfam: PF00111; fer2; 1.			
	DR	PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.			
	RW	Iron; Iron-sulfur protein.			
	SQ	SEQUENCE 113 AA; 11991 MW; 3E7F77A539F77276 CRC64;			
		Query Match 59.0%; Score 365; DB 2; Length 113;			
		Best Local Similarity 67.0%; Pred. No. 4.2e-29; Mismatches 14; Indels 0; Matches 67; Conservative 19;			
Qy	10	VTAIQTDERAYCAGSSESLLAGMARGRGRGIPVGCLNGGGVCKVRVLRGAVRKLG			
Db	11	DR 12 VTVQTGERFSCLAGMARGRGRGIPVGCLSGGGVCKVAVCVRGOSVRKG			
Qy	70	HVSAAEENDGYALACRYYVPGDVELEVAGRRLRKPFECGMA 109			
Db	71	DR 72 HISVEEAEQGVVLA CRVAPTDVVEVVKMQKEPFKGHS 111			
		CDOR.			
		GN Comamonas sp. JS765.			
	OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;			
	OC	Comamonadaceae; Comamonas.			
	OX	NCBI_TAXID:58226;			
	RN	[1] _			
	RP	SEQUENCE FROM N.A.			
	RC	STRAIN:JS765;			
	RX	Medline=98113817; PubMed=9451836;			
	RA	Parles R.E.; Ontl T.A.; Gibson D.T.;			
	RT	"Cloning and sequence analysis of a catechol 2,3-dioxygenase gene from the nitrobenzene-degrading strain Comamonas sp. JS765."			
	RT	J. Ind. Microbiol. Biotechnol. 18:385-391(1997).			
	RL	CC -; COFACTOR: BINDS 1 2FE-2S CLUSTER (BY SIMILARITY).			
	DR	EMBL: U93109; AAC79917.1; -.			
	DR	GO:0005849; P:electron transport activity; IEA.			
	DR	GO:0006118; P:electron transport; IEA.			

Q9S144	PRELIMINARY;	PRT;	118 AA.	DR Pfam; PF00111; fer2; 1.
AC Q9S144;				DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
DT 01-MAY-2000 (TREMBLrel. 13, Created)				DR Iron; Iron-sulfur.
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)				KW SEQUENCE 121 AA; 12722 MW; C29F512A0BDC749 CRC64;
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)				Query Match 52.2%; Score 323; DB 2;
DE Ferredoxin-like protein.				Best Local Similarity 64.6%; Pred. No. 7.6e-25;
GN PHCQ.				Matches 62; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
OS Comamonas testosteronei (Pseudomonas testosteronei);				
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;				
OC Comamonadaceae; Comamonas.				
NCBI TaxID=285;				
RP SEQUENCE FROM N.A.				
RC STRAIN=R5;				
RA MEDLINE=20055761; PubMed=10588844;				
RA Teramoto M., Furamata H., Harryama S., Watanabe K.;				
RT "Characterization of a high-affinity phenol hydroxylase from Comamonas				
RT testosteronei R5 by gene cloning, and expression in Pseudomonas				
RT aeruginosa PAO1.";				
RL Mol. Gen. Genet. 262:552-558 (1999).				
CC -1- COFACTOR: BINDS 1 2FE2S CLUSTER (BY SIMILARITY).				
DR BMBL; AB024741; BAA8774.1; -.				
DR GO; GO:0005489; F:electron transporter activity; IEA.				DT 01-MAY-1999 (TREMBLrel. 10, Created)
DR GO; GO:0006118; P:electron transport; IEA.				DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DR InterPro; IPR00658; 2FE2S fd BS.				DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DR InterPro; IPR001041; Ferredoxin.				DE Ferredoxin.
DR Pfam; PF00111; fer2; 1.				GN CBZT.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.				OS Pseudomonas putida.
DR Iron; Iron-sulfur.				OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonas.
KW Iron; Iron-sulfur.				OC Pseudomonadaceae; Pseudomonas.
SQ SEQUENCE 118 AA; 12480 MW; 583F12ACA8E6B74 CRC64;				OX NCBI_TaxID=303;
Query Match 52.2%; Score 323; DB 2;				RN [1]_TaxID=303;
Best Local Similarity 64.6%; Pred. No. 7.4e-25;				RP SEQUENCE FROM N.A.
Matches 62; Conservative 12; Mismatches 22; Indels 0; Gaps 0;				RC STRAIN=GJ31;
QY 10 VTIAGTDERYACVSGESLISLGMAGKLGRRGIPVGCLNGGCCVCKVRLGAVRKGPISA 69				RX MEDLINE=99138753; PubMed=9973359;
Db 6 VSVEQFDYACGTHEESLISLGMGRKGIPGCVNGGCCVCKVQLGAVRKGPVSCA 65				RA Mars A.E., Kingma J., Raschabek S.R., Reineke W., Janssen D.B.;
QY 70 HVSAEENNDDGYALACRVPPDGVLEVAQRKPF 105				RT "Conversion of 3-chlorocatechol to various catechol 2,3-dioxygenases and sequence analysis of the chlorocatechol dioxygenase region of
Db 66 HVSDDLERDQSYTLACRVALEAVRIAVAQRHLHKPF 101				RT and sequence analysis of the chlorocatechol dioxygenase region of
Query Match 52.2%; Score 323; DB 2;				RT pseudomonas putida GU31;"
Best Local Similarity 64.6%; Pred. No. 7.4e-25;				RL J. Bacteriol. 181:1309-1318 (1999).
Matches 62; Conservative 12; Mismatches 22; Indels 0; Gaps 0;				CC -1- COFACTOR: BINDS 1 2FE2S CLUSTER (BY SIMILARITY).
QY 10 VTIAGTDERYACVSGESLISLGMAGKLGRRGIPVGCLNGGCCVCKVRLGAVRKGPISA 69				DR EMBL; AF109301; ADD05249.1; -.
Db 6 VSVEQFDYACGTHEESLISLGMGRKGIPGCVNGGCCVCKVQLGAVRKGPVSCA 65				DR GO; GO:0005489; F:electron transporter activity; IEA.
QY 70 HVSAEENNDDGYALACRVPPDGVLEVAQRKPF 105				DR GO; GO:0006118; P:electron transport; IEA.
Db 66 HVSDDLERDQSYTLACRVALEAVRIAVAQRHLHKPF 101				DR InterPro; IPR006058; 2FE2S fd BS.
Query Match 52.2%; Score 323; DB 2;				DR InterPro; IPR001041; Ferredoxin.
Best Local Similarity 64.6%; Pred. No. 7.4e-25;				DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
Matches 62; Conservative 12; Mismatches 22; Indels 0; Gaps 0;				DR Pfam; PF00111; fer2; 1.
Q9ZNPI	PRELIMINARY;	PRT;	121 AA.	DR SEQUENCE 119 AA; 12747 MW; 12256EE66062F06 CRC64;
AC Q9ZNPI;				Query Match 52.0%; Score 322; DB 2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)				Best Local Similarity 56.4%; Pred. No. 9.4e-25;
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)				Matches 62; Conservative 13; Mismatches 35; Indels 0; Gaps 0;
DE Ferredoxin-like protein.				KW Iron; Iron-sulfur.
GN APHQ.				SEQUENCE 119 AA; 12747 MW; 12256EE66062F06 CRC64;
OS Comamonas testosteronei (Pseudomonas testosteronei);				QY 9 TVTIAGTDERYACVSGESLISLGMAGKLGRRGIPVGCLNGGCCVCKVRLGAVRKGPISA 68
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;				DR 10 SVTVMQTGETPECATDESLLQGMRLGRKGIPVGCVNGGCCVCKVQLGAVRKGPVSR 69
OC Comamonadaceae; Comamonas.				Query Match 69 AHVSAEENNDDGYALACRVPPDGVLEVAQRKPF 118
NCBI TaxID=225;				DR 70 AHVSAEAFARGFTLACRVAPEVTPVQLEVGKFEKFVSKGFVSTNNEINK 119
RP SEQUENCE FROM N.A.				RESULT 8
RC STRAIN=TA441;				Q9EXM1
DR GO; GO:0005489; F:electron transporter activity; IEA.				ID Q9EXM1; PRELIMINARY;
DR GO; GO:0006118; P:electron transport; IEA.				AC Q9EXM1;
DR InterPro; IPR006058; 2FE2S fd BS.				DT DT 01-MAR-2001 (TREMBLrel. 16, Created)
DR InterPro; IPR001041; Ferredoxin.				DT DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DR Chloroplast-type ferredoxin.				DT DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
GN ALND.				

DS	Escherichia coli.	Db	4 VKIDQTESEYCCNSNLSQSLQGNTQQLGRGIPVGCLNGCGVCKRILGEYRQ-GFMSRA 62
DC	Bacteriia; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	Qy	70 HVSAEEENDGYALACRVPDGDYVELEAGRILRK 102
RT	Enterobacteriaceae; Escherichia.	Db	63 HVSEDEQQRIVLACRVPDCSDVLSVYGMK 95
NCBI_TaxID=562;			
[1]	SEQUENCE FROM N.A.		
TRANSPONSON=IN5-Mob;		RESULT 10	
RC	MEDLINE=98276889; PubMed=9614705;	Q93JX0	PRELIMINARY;
RX	Murakami S., Nakashita Y., Kodama N., Takenaka S., Shinke R., Aoki K.;	ID	PRT; 111 AA.
RT	"Purification, characterization, and gene analysis of catechol 2,3-dioxygenase from the aniline-assimilating Pseudomonas species AW-2.";	AC	
RT	Biosci. Biotechnol. Biochem. 62:747-752 (1998).	DT	01-DEC-2001 (TREMBLrel. 19, Created)
RT	EMBL; AB040405; BAB18932.1; -.	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
RT	GO; GO:005489; GO:006118; Peletector transporter activity; IEA.	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
RT	InterPro; IPR006038; 2FE2S fd BS.	DE	Plant-type ferredoxin.
RT	InterPro; IPR001041; Ferredoxin.	GN	TDND2.
RT	Prosite; PS00197; 2FE2S_FERREDOXIN; 1.	OS	Pseudomonas putida.
RT	Iron; Iron-sulfur.	OG	Plasmid pT1N.
DR	SEQUENCE 91 AA; 9529 MW; BCF548719F903C5B CRC64;	OC	Bacteriia; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
DR	SEQUENCE 91 AA; 9529 MW; BCF548719F903C5B CRC64;	OC	Pseudomonadaceae; Pseudomonas.
DR	SEQUENCE 91 AA; 9529 MW; BCF548719F903C5B CRC64;	NCBI_TaxID=303;	
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	RN	SEQUENCE FROM N.A.
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	RA	Fukumori F.;
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	RL	REFRACTED (MAY-1996) to the EMBL/GenBank/DBJU databases.
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	CC	-1-COPARTICIPATOR: BINDS 1 2FE-S CLUSTER (BY SIMILARITY).
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	DR	EMBL; B85415; BA62049.1; -.
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	DR	GO; GO:0046841; C:extrachromosomal DNA; IEA.
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	DR	GO; GO:0005489; C:electron transporter activity; IEA.
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	DR	GO; GO:0006118; P:electron transport; IEA.
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	DR	DR InterPro; IPR006058; 2FE2S fd BS.
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	DR	DR InterPro; IPR001041; Ferredoxin.
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	DR	PFAM; PF00111; fer2.1.
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	DR	PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	DR	KW; Iron-sulfur; Plasmid.
DR	Query Match Score 48.8%; Best Local Similarity 64.7%; Pred. No. 7.2e-23; Matches 55; Conservative 12; Mismatches 18; Indels 0; Gaps 0;	SQ	SEQUENCE 111 AA; 11919 MW; OF517417F27AA9C7 CRC64;
DR	Query Match Score 43.2%; Best Local Similarity 55.3%; Pred. No. 2.6e-19; Matches 52; Conservative 15; Mismatches 24; Indels 3; Gaps 1;	Qy	10 VTIATQTDERYACYSGESLIIAGMAGLRRGIPVGCLNGCGVCKRVLRA-VRKGPISR 68
DR	Query Match Score 43.2%; Best Local Similarity 55.3%; Pred. No. 2.6e-19; Matches 52; Conservative 15; Mismatches 24; Indels 3; Gaps 1;	Db	6 ICIDTGEYACASRSRVSLEGMAEKGKGIPVGCRGGCGVCKRVLLEGQYVRRV-MSR 63
DR	Query Match Score 43.2%; Best Local Similarity 55.3%; Pred. No. 2.6e-19; Matches 52; Conservative 15; Mismatches 24; Indels 3; Gaps 1;	Qy	69 AHVSAEEENDGYALACRVPDGDYVELEAGRILRK 102
DR	Query Match Score 43.2%; Best Local Similarity 55.3%; Pred. No. 2.6e-19; Matches 52; Conservative 15; Mismatches 24; Indels 3; Gaps 1;	Db	64 AHVSAEEAGCALSCRIPSSDRLQLVIGAMK 97
DR	SEQUENCE FROM N.A.	RESULT 11	
DR	SEQUENCE FROM N.A.	Q93JX0	PRELIMINARY;
DR	SEQUENCE FROM N.A.	ID	PRT; 101 AA.
DR	SEQUENCE FROM N.A.	AC	
DR	SEQUENCE FROM N.A.	DT	01-NOV-1998 (TREMBLrel. 08, Created)
DR	SEQUENCE FROM N.A.	DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DR	SEQUENCE FROM N.A.	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DR	SEQUENCE FROM N.A.	DE	Chloroplast-type ferredoxin.
DR	SEQUENCE FROM N.A.	DE	PANTHI.
DR	SEQUENCE FROM N.A.	GN	Burkholderia sp. RP007.
DR	SEQUENCE FROM N.A.	GN	Bacteriia; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia.
DR	SEQUENCE FROM N.A.	NCBI_TaxID=83784;	NCBI_TaxID=83784;
DR	SEQUENCE FROM N.A.	RN	Ralstonia sp. E2.
DR	SEQUENCE FROM N.A.	RP	Bacteriia; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia.
DR	SEQUENCE FROM N.A.	RC	OC
DR	SEQUENCE FROM N.A.	RC	OC
DR	SEQUENCE FROM N.A.	RC	NCBI_TaxID=6739;
DR	SEQUENCE FROM N.A.	RC	SEQUENCE FROM N.A.
DR	SEQUENCE FROM N.A.	RC	STRAIN=E2;
DR	SEQUENCE FROM N.A.	RC	MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
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DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
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DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
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DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
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DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	DR MEDLINE=93361023; PubMed=9695910;
DR	SEQUENCE FROM N.A.	RC	RA Hino S., Watanabe K., Takahashi N.;
DR	SEQUENCE FROM N.A.	RC	"phenol hydroxylase cloned from Ralstonia eutropha strain E2 exhibits novel kinetic properties."
DR	SEQUENCE FROM N.A.	RC	Microbiology 144:0-0(0).
DR	SEQUENCE FROM N.A.	RC	-1-COPARTICIPATOR: AAC32458.1; -.
DR	SEQUENCE FROM N.A.	RC	EMBL; AF026065; AAC32458.1; -.
DR</td			

DR	HSSP; P56408; 1AWD.	DT	01-JUN-2001 (TREMBLrel. 17, Created)
DR	GO; GO:0005489; F:electron transporter activity; IEA.	DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DR	GO; GO:0006118; P:electron transport; IEA.	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DR	InterPro; IPR00058; 2Fe2S fd BS.	DB	Probable plant-type ferredoxin.
DR	InterPro; IPR001041; Ferredoxin.	GN	XVLT.
PFam	PF00111; fer2; 1.	OS	Pseudomonas sp. S-47.
DR	PROSITE; PS00119; 2Fe2S_FERREDOXIN; 1.	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonades.
DR	Iron; Iron-sulfur.	OC	Pseudomonadaceae; Pseudomonas.
SW	SEQUENCE 101 AA; 10833 MW; 7A7EA53B831C15D CRC64;	OX	NCBI_TAXID=115714;
Query Match	36.9%; Score 228.5; DB 2; Length 101;	RN	
Best Local Similarity	48.9%; Pred. No. 28-15; 12; Mismatches 35; Indels 1; Gaps 1;	RN	SEQUENCE FROM N.A.
Matches	46; Conservative 12; Mismatches 35; Indels 1; Gaps 1;	RA	Park D.-W., Kim C.-K.;
QY	9 TTVIAQTERYACVSGHSEILLAGMAKLRGKIPVGCLNGGCVCKVRVLRGAVRKLGPIRSR 68	RA	Lee S.-M., Ka J.-O., Kim C.-K.;
DB	3 TVEIAQSGQYPCDPCGQNLIRLAKAFAFPDSDIRLPAALLAR 95	RT	Cloning and Sequence Analysis of the xyL Gene Responsible for 4CBA-
QY	69 AHVSAEBBENDGYALACRQVPGDVELEVAAGRRLRK 102	DR	Dihydrodiol Dehydrogenase from Pseudomonas sp. S-47.";
DB	62 ACLSEAEQQGSVLIQVAKAFAFPDSDIRLPAALLAR 95	DR	Microbiol. 38:275-280 (2000).
RESULT 12		DR	[2]
Q9RAF3	PRELIMINARY; PRT; 115 AA.	DR	RP SEQUENCE FROM N.A.
ID	Q9RAF3	DR	PARK, D.-W.; KIM, C.-K.;
AC	Q9RAF3;	DR	Submitted (EBB-2002) to the EMBL/GenBank/DBJ databases.
DT	01-MAY-2000 (TREMBLrel. 13, Created)	DR	EMBL; AF320881; AAC0803-2; -
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DR	GO; GO:0005489; F:electron transporter activity; IEA.
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DR	GO; GO:0006118; P:electron transport; IEA.
DR	InterPro; IPR006058; 2Fe2S fd BS.	DR	InterPro; IPR006058; 2Fe2S fd BS.
DR	InterPro; IPR001041; Ferredoxin.	DR	InterPro; IPR001041; Ferredoxin.
DR	PFam; PF00111; fer2; 1.	DR	PFam; PF00111; fer2; 1.
DR	PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.	DR	PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
QY	17 ERYACVSGESLQAGMAKLRGKIPVGCLNGGCVCKVRVLRGAVRKLGPIRSRHSVSAPEE 76	DR	Best Local Similarity 33.2%; Score 205.5; DB 2; Length 112;
DB	15 QSFRCAGQSIVRAMEAQGKRCIPVGGCRGGCCCLCRVRLSGARYS-GRMSRSHVPAKAA 73	DR	Mismatches 39; Conservative 14; Gaps 1; Indels 1; Gaps
QY	77 NDGYALACRQVPGDVELE 95	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;
DB	74 AEGFALACQVFQFDLTIE 92	DR	Query Match
RESULT 14		DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;
Q45344	PRELIMINARY; PRT; 119 AA.	DR	Mismatches 25; Indels 1; Gaps
ID	Q45344;	DR	Q45344;
AC	Q45344;	DR	Score 205.5; DB 2; Length 112;
DT	01-NCV-1996 (TREMBLrel. 01, Created)	DR	Match
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DR	Mismatches 25; Indels 1; Gaps
DR	Chloroplast-type ferredoxin.	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;
DR	TB0W.	DR	Query Match
OS	Burkholderia pickettii (Pseudomonas pickettii).	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;
CC	Burkholderia; Proteobacteria; Betaproteobacteria; Burkholderiales;	DR	Mismatches 25; Indels 1; Gaps
OC	Ralstonia sp. KNL.	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;
OC	Burkholderiaceae; Ralstonia.	DR	Query Match
OX	NCBI_TAXID=103439;	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;
RN		DR	Mismatches 25; Indels 1; Gaps
RC	SEQUENCE FROM N.A.	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;
RC	"Constitutive trichloroethylene degradation led by tac promoter chromosomally integrated upstream of phenol hydroxylate genes of Ralstonia sp. KNL and its nucleotide sequence analysis.";	DR	Query Match
RT	Ralstonia sp. KNL and its nucleotide sequence analysis.";	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;
RT	J. Biosci. Bioeng. 89:47-54 (2000).	DR	Mismatches 25; Indels 1; Gaps
CC	-1-COFACTOR: BINDS 1.2FE-2S CLUSTER (BY SIMILARITY).	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0D365AE226 CRC64;	
DR	DR	Query Match	
DR	DR	Best Local Similarity 49.4%; Pred. No. 4.5e-13;	
DR	DR	Mismatches 25; Indels 1; Gaps	
DR	DR	SEQUENCE 112 AA; 12054 MW; 799D4F0	

Query Match 32.9%; Score 203.5; DB 2; Length 119;
 Best Local Similarity 51.0%; Pred. No. 7.7e-13; Indels 11; Gaps 3;
 Matches 49; Conservative 6; Mismatches 30;

QY 28 LAGMAKLGRRGIPVGGLNGGGVCKVRLGAVRKLG----PISRAHVSAAEENDGYAL 82
 Db 28 LTGMLRLGRRGIPVGCGVCKVRLGDSR-LGRRQCPQRSSA---GLTL 81

QY 83 ACRVVPDGDVELEVAGRRLRKBFECGMACAGTAAINK 118
 Db 82 ACRAEPLTAVRLAVLKGKFERFSSRASAFAGAQSDTK 117

RESULT 15

Q847GB PRELIMINARY; PRT; 105 AA.

ID Q847GB; AC Q847GB; DT 01-JUN-2003 (TRIMBLref. 24, Created)
 DT 01-JUN-2003 (TRIMBLref. 24, Last sequence update)
 DT 01-OCT-2003 (TRIMBLref. 25, Last annotation update)
 DE Ferredoxin.
 GN NAHT.
 OS Pseudomonas putida.
 OC Plasmid pPFG1.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Pseudomonas.
 OC NCBI_TAXID=303;

FN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-NCIB 9816-4;
 RA Zylstra, G.J., Dennis, J.J.;
 RT "Complete nucleotide sequence of the NAH plasmid pPTG1 from
 Pseudomonas putida NCIB 9816-4."
 RT Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AR491207; AAO64106.1;
 DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO: GO:0005489; F:electron transport; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR00658; 2FE2s fd.BS.
 DR InterPro; IPR001041; Ferredoxin.
 DR Pfam: PF00111; fer2; 1
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
 DR Plasmid.
 SQ SEQUENCE 105 AA; 11344 MW; 48568FAC91D640BD CRC64;
 SQ 30.5%; Score 189; DB 2; Length 105;
 Best Local Similarity 42.6%; Pred. No. 1.9e-11; Indels 4; Gaps 2;
 Matches 40; Conservative 16; Mismatches 34;

QY 10 VTIAQTDERYACYSGESLIIAGMAKLGRRGIPVGCGVCKVRLGAVRKLGPIRSA 69
 Db 7 ITVOQGGEREFAQPLQSVLSAMETQGKQCLPVGERGGCGLCKVRLLAGDY-ECGRVSCK 65

QY 70 HVSAEEENGYALACRVVPGDVELEVAGRRLRK 103
 Db 66 HLPYEAEEQYALACRLFARSDLCLIE--RYSKP 96

Search completed: August 5, 2004, 13:16:54
 Job time : 40 secs